

Jarrell, Noble

181606

From: Ramirez, Delia  
Sent: Tuesday, March 07, 2006 5:49 PM  
To: Jarrell, Noble  
Subject: 09/541,462

Hi,

I would like to request the following search:

1. an oligo search (at least 12 nucleotides long) of SEQ ID NO:1 and 2 in the nucleic acid databases (commercial only)

Thank you very much,

---

Delia M. Ramirez, Ph.D.  
Patent Examiner  
Recombinant Enzymes-Art Unit 1652  
USPTO  
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70  
Alexandria, VA 22314  
(571) 272-0938  
delia.ramirez@uspto.gov

Noble  
Fin 3/16/06

4 NNA oligo  
20PR compugen  
20 one

**This Page Blank (uspto)**

**Jarrell, Noble**

---

**From:** Ramirez, Delia  
**Sent:** Tuesday, March 07, 2006 5:44 PM  
**To:** Jarrell, Noble  
**Subject:** 09/541,462

Hi,

I would like to request the following INTERFERENCE search:

1. SEQ ID NO:1 and 2 in the nucleic acid databases.
2. an oligo search (at least 12 nucleotides long) of SEQ ID NO:1 and 2 in the nucleic acid databases.

Thank you very much,

---

Delia M. Ramirez, Ph.D.  
Patent Examiner  
Recombinant Enzymes-Art Unit 1652  
USPTO  
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70  
Alexandria, VA 22314  
(571) 272-0938  
[delia.ramirez@uspto.gov](mailto:delia.ramirez@uspto.gov)

This Page Blank (Use Back)



LENGTH: 432  
; TYPE: DNA  
; ORGANISM: zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(432)  
; OTHER INFORMATION: Ceres Seq. ID no. 4776740  
US-11-096-568A-14405

Alignment Scores:  
Pred. No.: 2.64e-67 Length: 432  
Score: 70.00 Matches: 70  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 64.8% Indels: 0  
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) × US-11-096-568A-14405 (1-432)

Qy 29 AlaValAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaIleCysArgAsnHis 48  
Db 188 GCGGTCGCTCTGGCTGGATATCGTGTGCAATTGCCCATCTGCAGAACCC 247

Qy 49 IleMetAspIleCysIleIleGluCysGlnAlaAsnGlnAlaSerIleThrSerGluGluCys 68  
Db 248 ATCATGGATCTGATGATGATGTCAGGCTTAATCGGCCAGGGCTAACAGTGAGGAATGC 307

Qy 69 ThrValAlaTrpGlyIleValCysAsnHisAlaPheHisPheHisCysIleSerArgTriple 88  
Db 308 ACTGTTGCTTGGGCTTTGAAATCAGCCCTCCACTTCACGTCAAGATGGTTA 367

Qy 89 LysThrArgIleGlnValCysProIleAspAsn 98  
Db 368 AAGACTCTGTCAGTTGCCATTGTAAAC 397

RESULT 3  
US-11-096-568A-26820  
; Sequence 26820, Application US/11096568A  
; GENERAL INFORMATION:  
; Publication No. US2006048240A1  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 26820  
; LENGTH: 693  
; TYPE: DNA  
; ORGANISM: zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(693)  
; OTHER INFORMATION: Ceres Seq. ID no. 13622871  
US-11-096-568A-26820

Alignment Scores:  
Pred. No.: 2.29e-36 Length: 693  
Score: 42.00 Matches: 42  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 38.9% Indels: 0  
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) × US-11-096-568A-26820 (1-693)

Qy 32 LeuTrpAlaTrpAspIleValAspAsnCysAlaIleCysArgAsnHisIleMetAsp 51  
Db 207 CTCTGGCCCTGGACATCGTGTGGAACTSGGCCATCTGCGCCAACCATGAGAC 266

Qy 52 LeuCysIleGluCysGlnAlaAsnGlnAlaSerIleThrSerGluGluCysThrValAla 71

Db 267 CTCTGCATCGAGTCCAGGGAAACAGGGAGGCCACAGCGAGGTGACCGTCGCT 326

Qy 72 TrpIleY 73  
Db 327 TGGCGA 332

RESULT 4  
US-11-096-568A-28569  
; Sequence 28569, Application US/11096568A  
; Publication No. US2006044240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 28569  
; LENGTH: 348  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(348)  
; OTHER INFORMATION: Ceres Seq. ID no. 3017472  
US-11-096-568A-28569

Alignment Scores:  
Pred. No.: 2.07e-34 Length: 348  
Score: 40.00 Matches: 68  
Percent Similarity: 97.1% Conservativeness: 0  
Best Local Similarity: 97.1% Mismatches: 1  
Query Match: 37.0% Indels: 2  
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) × US-11-096-568A-28569 (1-348)

Qy 29 AlaValAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaIleCysArgAsnHis 48  
Db 106 GCTGCGCTCTGGCTTGGATACTGTTGTTGATACTGCGATTGTTGAGATCAC 165

Qy 49 IleMetAspIleCysIleGluCysGlnAlaSerIleAlaSerIleThrSerGluGluCys 68  
Db 166 ATCAGGATCTCTTGTGATGATGCTT-AGCTAAATCAAGCTGACTGAGGAATG 224

Qy 68 sThrValAlaIleGluCysAsnHisAlaPheHisPhHisCysIleSerArgTriple 88  
Db 225 CACTGTTGCTGGGGTTGCAACCGCTTCACTTCACCTGATGAGATGGCT 284

Qy 88 uLysThrArgGlnValCysProIleAsp 97  
Db 285 CAAACTCGTCAGTGTCCACTAGAT 312

RESULT 5  
US-10-932-182A-81177/C  
; Sequence 81177, Application US/10932182A  
; Publication No. US200604653A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: KODAMA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 81177  
; LENGTH: 153  
; TYPE: DNA

ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-81177

## Alignment Scores:

Pred. No.: 0 0.000629 Length: 153  
Score: 12.00 Matches: 12  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Missmatches: 0  
Query Match: 11.1% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-81177 (1-153)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50  
Db 68 GTTGACACTGTGCTATTGGAGAACATAATG 33

## RESULT 6

US-10-932-182A-81177/c  
Sequence 81177, Application US/10932182A  
Publication No. US20060046253A1  
GENERAL INFORMATION:  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHIWA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: 030685-043  
CURRENT APPLICATION NUMBER: US/10/932,182A  
CURRENT FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 81177  
LENGTH: 153  
TYPE: DNA  
ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-81177

## Alignment Scores:

Pred. No.: 0 0.000629 Length: 153  
Score: 12.00 Matches: 12  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Missmatches: 0  
Query Match: 11.1% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-81177 (1-153)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50  
Db 68 GTTGACACTGTGCTATTGGAGAACATAATG 33

## RESULT 7

US-10-932-182A-6146/c  
Sequence 6146, Application US/10932182A  
Publication No. US20060046253A1  
GENERAL INFORMATION:  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHIWA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: 030685-043  
CURRENT APPLICATION NUMBER: US/10/932,182A  
CURRENT FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 6146  
LENGTH: 207  
TYPE: DNA  
ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-2279

```

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTTATTCAGAACCATATG 189

RESULT 10
US-10-932-182A-78459
; Sequence 78459, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 78459
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78459

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTTATTCAGAACCATATG 189

RESULT 11
US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIWA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279

```

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame\_plus\_P2n model

Run on: March 11, 2006 08:24:33 ; Search time 653 Seconds  
(without alignments)

Scoring table: BLOSUM62

Title:	US-09-541-462B-2	
Perfect score:	616	
Sequence:	1 MAAMDVDTPTSGTNSGACKK.....KTRQVCPLDNREWEFQYGH 108	
Xgapop	10.0 , Ygapext	0.5
Ygapop	10.0 , Ygapext	0.5
Fgapop	6.0 , Fgapext	7.0
Delop	6.0 , Delext	7.0

Searched: 9793542 seqs, 4134669005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

```
-MODE=frame_plus_model -DEV=x1h
-Q=/abs/ABSSWEB_spool/US09541462/runat_10032006_080735_22137/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFM=rfpm -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCH=0 -LOOPEXT=0 -UNITS=bis -START=-1 -END=-1 -MATRIX=blossum62
-TRANS=human40.cdd -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFORMAT=pto -NORMnext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000 -HOST=bbsbnsh
-USER=US09541462 @CGN_1_1_1026 @runat_10032006_080735_22137 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=10 -LONGLOG -DEVTIMOUT=120
-WARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DDELOP=6 -DELEXT=7
```

Database :

```
Published Applications_NA_Main:*
1: /cgnz_6/ptodata/1/pubna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	433	7	US-10-085-783A-57254
2	616	100.0	433	7	US-10-085-535A-56068
3	616	100.0	453	7	US-10-085-783A-56068
4	616	100.0	453	7	US-10-085-783A-43377
5	616	100.0	467	7	US-10-085-783A-43377
6	616	100.0	467	7	US-10-085-783A-43377
7	616	100.0	471	7	US-10-085-783A-43377

**ALIGNMENTS**

RESULT 1  
US-10-242-535A-43377 ; Sequence 43377, Application US/10242535A

; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY OR AGENT: Lieuw, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085-783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO: 43377  
; LENGTH: 433  
; TYPE: DNA  
; ORGANISM: Human  
US-10-242-535A-43377

Alignment Scores:  
Pred. No.: Score: 39333, A  
Score: 39333, A  
Percent Similarity: 100.0%

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	433	7	Sequence 43377, A
2	616	100.0	433	7	Sequence 43377, A
3	616	100.0	453	7	Sequence 35025, A
4	616	100.0	453	7	Sequence 35025, A
5	616	100.0	467	7	Sequence 39333, A
6	616	100.0	467	7	Sequence 39333, A
7	616	100.0	471	7	Sequence 57254, A

Length: 433  
Matches: 108  
Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-43377 (1-433)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 20 ATGGCGCAGGGATGATGTGATAACCCACAGGGCGGGAAAGAG 79

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
 Db 80 CGCTTGAAGTGAAGAAAAAGTCGAATCGAACGCCCTCGGCCATGGATATTGTCTTTGAT 139

Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
 Db 140 AACTGTGCCATCTGCAAGGACCCTTGATTTGCATAATGCAATGGATTTGAC 199

RESULT 3  
 US-10-242-535A-35025  
 ; Sequence 35025, Application US/10242535A  
 ; Publication No. US20040013663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2005  
 ; CURRENT APPLICATION NUMBER: US/10/242,535A  
 ; CURRENT FILING DATE: 2002-09-12  
 ; PRIORITY APPLICATION NUMBER: US 10/085,783  
 ; PRIORITY FILING DATE: 2002-02-28  
 ; PRIORITY APPLICATION NUMBER: US 60/305,340  
 ; PRIORITY FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIORITY FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/275,955  
 ; PRIORITY FILING DATE: 2002-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO: 35025

Qy 61 AlaSerAlaThrSerGluCysTrpAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 200 GCGTGGCTACTCACCATGTCAGATGTCAGCTAACGCTAAC 259

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 260 TTCCACTGCATCTCGCTGTCATTGGCAACAGGAG 319

Qy 101 TrpGlutpheGlnLysTrpGlyHis 108  
 Db 320 TGGGAATTCCAAAAGTATGGCAC 343

RESULT 2  
 US-10-085-783A-43377  
 ; Sequence 43377, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; PRIORITY FILING DATE: 2002-02-28  
 ; PRIORITY APPLICATION NUMBER: US 60/305,340  
 ; PRIORITY FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIORITY FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO: 43377  
 ; LENGTH: 433  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-085-783A-43377

Alignment Scores:  
 Pred. No.: 2.71e-14 Length: 433  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-43377 (1-433)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 20 ATGGCGCAGGGATGATGTGATAACCCACAGGGCGGGCAAGAG 79

Alignment Scores:  
 Pred. No.: 2.71e-14 Length: 433  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-43377 (1-433)

Qy 61 AlaSerAlaThrSerGluCysTrpAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 204 GCGTGGCTACTTCACAGGTACTGTGGACTCTGAACCATGCTTCAC 263

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 264 TTCCACTGCATCTCGCTGGCTAACACAGCAACAGGAG 323



ORGANISM: Human  
US-10-085-783A-39933

Alignment Scores:  
Pred. No.: 3.01e-74 Length: 467  
Score: 616.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 40  
Best Local Similarity: 100.0% Minmatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-39933 (1-467)

QY 1 MetAlaAlaAlaValAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
Db 17 ATGCCGGCAGCGATGGTGGACTGGTAAACCCGAGGGCAACGGGGCCAAAGAG 76

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeutrpAlaTrpAspIleValValAsp 40  
Db 77 CGCTTGAACTGGTAAAGTGGAAATGGATGCAGTAGCCCTCTGGCTGGATATTGTGTTGAT 136

QY 41 AsnCysAlaIleCysArgAsnHisIleLeuAspIleCysGlnAlaAsnGln 60  
Db 137 AACGTGCCCCATTCAGGACCACATTGGATTTGATAAGATGTCAGCTAACAGAG 196

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHis 80  
Db 197 GCGTCGGTACTCAGACTGCACTGGATGGCTTAACCATGCTTTCAC 256

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgInvaIleCysProLeuAspAsnArgGlu 100  
Db 257 TTCCACTGCATCTCGTGGTCAAAACAGAACAGAG 316

QY 101 TrpGluPheGlnIleStryGlyHis 108  
Db 317 TGGAAATTCCAAGAAGTATGGCAC 340

RESULT 8  
US-10-085-783A-57254  
; Sequence 57254, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; INVENTOR: Liaw, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; CURRENT FILING DATE: 2002-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 57254  
; LENGTH: 471  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/102442535A  
; PRIOR APPLICATION NUMBER: US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; INVENTOR: Liaw, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; PRIOR APPLICATION NUMBER: US 10-085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 57254  
; LENGTH: 471  
; TYPE: DNA  
; ORGANISM: Human  
US-10-242-535A-57254

Alignment Scores:  
Pred. No.: 3.05e-74 Length: 471  
Score: 616.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 40  
Best Local Similarity: 100.0% Minmatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-57254 (1-471)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
Db 17 ATGCCGGCAGCGATGGTGGACTGGTAAACCCGAGGGCAACGGGGCCAAAGAG 76

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeutrpAlaTrpAspIleValValAsp 40  
Db 77 CGCTTGAACTGGTAAAGTGGAAATGGATGCAGTAGCCCTCTGGCTGGATATTGTGTTGAT 136

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspIleCysGlnAlaAsnGln 60  
Db 137 AACGTGCCCCATTCAGGACCACATTGGATTTGATAAGATGTCAGCTAACAGAG 196

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHis 80

Db 197 GGTCCCTACTTCAGAGTGTACTGGGATCGTAACTGCTTAC 256  
 Qy 81 PheHisCysIleSerArgTrpLeuIleThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 257 TTCACTGCATCTCTGGTCATAACAGACAGTGTCATTGGACAACAGAG 316  
 Qy 101 TrpGlpheGinLysIleThrGlyHis 108  
 Db 317 TGGAAATCCAAAGTAGGGCAC 340

RESULT 9  
 US-10-242-535A-56068  
 ; Sequence 56068, Application US/10242535A  
 ; Publication No. US20040013663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; ATTORNEY: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; CURRENT APPLICATION NUMBER: US/10/242,535A  
 ; CURRENT FILING DATE: 2002-09-12  
 ; PRIOR APPLICATION NUMBER: US 10/085,783  
 ; PRIOR FILING DATE: 2002-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-02-08  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 56068  
 ; LENGTH: 472  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (437)..(437)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (455)..(455)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (437)..(437)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (455)..(455)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (437)..(437)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (455)..(455)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 US-10-242-535A-56068

Alignment Scores:  
 Pred. No.: 3.06e-74 Length: 472  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-085-783A-56068 (1-472)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20.  
 Db 20 ATGGCCGAGGGATGGATGGATACCCTGGCCACCAAGGGCGGGCAAGAG 79  
 Qy 21 ArgPheGluValLysIleSrrPAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40  
 Db 80 CGCTTGAGTGAAGTGAAGAAAATGGAATCAGTGCCCTGGCATTTGTCCTGAT 139  
 Qy 1 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
 Db 20 AACCTGCCATCTGCCAGAACCAATTATGCAATTGTCAGATGTCAAGCTAACCG 199  
 Qy 61 AlaserAlaThrSerGluGlyIleSerArgTrpLeuIleThrArgGlnValCysAsnHisAlaPheHis 80  
 Db 200 GCGTCGGTACTTCAGAAGGTGTACTGTCGTCATGGGACTCTGTAACCATGCTTTCAC 259  
 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
 Db 140 AACCTGCCATCTGCCAGAACCAATTATGCAATTGTCAGATGTCAAGCTAACCG 199  
 Qy 61 AlaserAlaThrSerGluGlyIleSerArgTrpLeuIleThrArgGlnValCysAsnHisAlaPheHis 80  
 Db 200 GCGTCGGTACTTCAGAAGGTGTACTGTCGTCATGGGACTCTGTAACCATGCTTTCAC 259  
 Qy 81 PheHisCysIleSerArgTrpLeuIleThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 260 TTCACTGCATCTGCCGTCATGGGACTCTGTCAGATGTCAAGCTAACCG 319  
 Qy 101 TrpGlpheGinLysIleThrGlyHis 108  
 Db 320 TGGAAATCCAAAGTAGGGCAC 343

RESULT 11  
US-10-913-937-5  
Sequence 5, Application US/10913937  
Publication No. US20050019813A1  
GENERAL INFORMATION:  
APPLICANT: Conway, Joan A.  
APPLICANT: Conway, Ronald C.  
APPLICANT: Kamura, Takumi  
APPLICANT: Oklamoma Medical Research Foundation  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/10/913,937  
CURRENT FILING DATE: 2004-08-05  
PRIORITY APPLICATION NUMBER: US/09/914,324  
PRIOR FILING DATE: 2001-08-22  
PRIORITY APPLICATION NUMBER: US 60/121,787  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/10/913,937  
CURRENT FILING DATE: 2004-08-05  
PRIORITY APPLICATION NUMBER: US/09/914,324  
PRIOR FILING DATE: 2001-08-22  
PRIORITY APPLICATION NUMBER: US 60/121,787  
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/10/913,937  
CURRENT FILING DATE: 2004-08-05  
PRIORITY APPLICATION NUMBER: WO PCT/US00/04838  
PRIOR FILING DATE: 1999-05-26  
PRIORITY APPLICATION NUMBER: WO PCT/US00/04838  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 504  
TYPE: DNA  
ORGANISM: Mus sp.  
FEATURE: CDS  
NAME/KEY: CDS  
LOCATION: (18)..(344)  
OTHER INFORMATION: Rbx1  
US-10-913-937-5

Alignment Scores:  
Pred. No.: 3.35e-74 Length: 504  
Score: 616.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 8 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-913-937-3 (1-508)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
DB 7 ATGGCGGAAGCGATGGATCTGGATAACCCGAGGCCAACACGGCCGGAAAGARG 66

QY 21 ArgpheGluValLysLysTrpAspAlaValAlaLeutrpAlaTrpAspIleValValasp 40  
DB 67 CGCTTGAAAGTGAAGATGGAAAGTGGAAATGGCAATGGCTAGCCCCTGGCCCTGGGATATTGCGTTGAT 126

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsnGin 60  
DB 127 AACGTGGCCATCTCAGAACCAATTGGATTTGATGATGTAAGCTAACATGCTTTCAC 186

QY 61 AlaSerAlaThrSerGluCysThrValAlaLeutrpGlyvalCysAsnHisAlaPheHis 80  
DB 187 GCGCCCGGTACTTCAGAACCAATTGGATTTGATGATGTAAGCTAACATGCTTTCAC 246

QY 81 PheIleCystIleSerArgTrpLeuLysThrArgLysValCysProlLeuAspAspArgGlu 100  
DB 247 TTCCACTGATCTCCTGCTGGCTAAACAGCACAGGCTGTGTCATTGGACACAGAG 306

QY 101 TrpGluPheGlnLysTrpGlyHis 108  
DB 307 TGGGACTTCAGAAAGTGGCCAT 330

RESULT 13  
US-10-242-535A-46292  
Sequence 46292, Application US/10242535A  
Publication No. US0040019663A1  
GENERAL INFORMATION:  
APPLICANT: ChondroGene Inc.  
APPLICANT: Liev, C.C.  
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
FILE REFERENCE: 4231/2005

RESULT 12  
US-10-913-937-3  
Sequence 3, Application US/10913937  
Publication No. US20050019813A1  
GENERAL INFORMATION:  
APPLICANT: Conway, Joan A.

PRIOR APPLICATION NUMBER: US 60/305,340  
*i* PRIOR FILING DATE: 2001-07-13  
*i* PRIOR APPLICATION NUMBER: US 60/275,017  
*i* PRIOR APPLICATION NUMBER: US 2001-03-12  
*i* PRIOR FILING DATE: 2001-03-12  
*i* PRIOR APPLICATION NUMBER: US 60/271,955  
*i* PRIOR FILING DATE: 2001-02-28  
*i* NUMBER OF SEQ ID NOS: 58994  
*i* SOFTWARE: PatentIn version 3.2  
*i* SEQ ID NO: 46292  
*i* LENGTH: 523  
*i* TYPE: DNA  
*i* ORGANISM: Human  
US-10-242-535A-46292

Alignment Scores:  
Pred. No.: 3.52e-74 Length: 523  
Score: 616.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-085-783A-46292 (1-523)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
Db 19 ATGGCGCAGCGATGCTGTGATAACCCGAGCCACCAACAGCGCCGCCAACAG 78

Alignment Scores:  
Pred. No.: 3.52e-74 Length: 523  
Score: 616.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-242-535A-46292 (1-523)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
Db 19 ATGGCGCAGCGATGCTGTGATAACCCGAGCCACCAACAGCGCCGCCAACAG 78

Qy 21 ArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
Db 79 CGCTTGAAAGTGAAGTGAAGTGAAGTGAATGTCATGGCTGGCATATGTGTTGAT 138

Qy 41 AsnCysValAlaLeuCysArgAspAspHisIleMetAspLeuCysIleGlucysGlnAlaAsnGln 60  
Db 139 AACCTGTCCTCATCTGAGAACCATATTGATCTTGCATAGATGCTAACAG 198

Qy 61 AlaSerAlaThrSerGluGlyCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
Db 199 GCTGCGCTACTTCGAAAGGTGACTGTGCGATGGGAGTCGTTTCAC 258

Qy 81 PheHisCysValLeuArgTrpLeuIleValCysProLeuAspAsnArgGlu 100  
Db 259 TTCCCACTGCATCTCTGCTCTCAAACAGCACAGGTGTGTCATTGGACAACAGAG 318

Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
Db 319 TGGGAATTCAAAAGATGGCAC 342

RESULT 14 US-09-918-995-17191  
*i* Sequence 17191, Application US/09918995  
*i* Publication No. US20030073623A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: HySeq, Inc.  
*i* TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
*i* FROM VARIOUS CDNA LIBRARIES  
*i* FILE REFERENCE: 20411-756  
*i* CURRENT APPLICATION NUMBER: US/09/918,995  
*i* CURRENT FILING DATE: 2001-07-30  
*i* PRIOR APPLICATION NUMBER: US/09/235,076  
*i* PRIOR FILING DATE: 1999-01-20  
*i* NUMBER OF SEQ ID NOS: 38054  
*i* SOFTWARE: FastSeq for Windows Version 3.0  
*i* SEQ ID NO: 17191  
*i* LENGTH: 476  
*i* TYPE: DNA  
*i* ORGANISM: Homo sapiens  
*i* FEATURE:  
*i* NAME/KEY: misc\_feature  
*i* LOCATION: (1) ..(476)  
*i* OTHER INFORMATION: n = A,T,C or G

US-09-541-462B-2 (1-108) × US-09-918-995-17191 (1-476)

Qy 2 AlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysLys 21  
Db 75 GCGCCAGCGATGCTGTGATAACCCGAGGGCACCAACAGCGCCGCCAACAGGCC 134

Qy	22	PheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsn	41
Db	135	TTCGAAGTGAAGAAATGGATGGATGGCTCGCCGGATAATGGGTGATAAC	194
Qy	42	CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla	61
Db	195	TGTGCCATCTGCACCAACCACATTGATCTTGATAGAACATCTAGCTAACAGCG	254
Qy	62	SerAlaThrSerGluGlucysIleValAlaIleTrpGlyValCysAsnHisAlaPheHisIle	81
Db	255	TCCGCTACTCTCAGAAGCTACTGCTGATGGGAGCTGTAAACCAGCTTTTCACTTC	314
Qy	82	HisCysIleSerArgTripleuLysThrArgGlnAlaValCysProLeuAspAsnArgGluTrp	101
Db	315	CACTGCATCTCTCGTGGCTCAAACACAGGGCATGGACATGGACACAGAGGG	374
Qy	102	GluPheGlnLysTrpGlyHis	108
Db	375	GAATTCAAAAGTATGGGCAC	395

Search completed: March 11, 2006, 08:38:02  
 Job time : 656 secs

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 15, 2006, 08:51:24 ; Search time 2486 Seconds  
(without alignments)

Perfect score: 108

Title: US-09-541-462B-2

Sequence: 1 MAAMDVDTPSGTNSGAGKK.....KTRQVCPILDNREWEFQKYGH 108

Scoring table: Oligo

Xgapext	60.0	Xgapext	60.0
Ygapext	60.0	Ygapext	60.0
Fgapext	6.0	Fgapext	7.0
DelOp	6.0	Delext	7.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 12

Total number of hits satisfying chosen parameters: 144

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+ P2n.model -DEV=x1P
-O=/abss/ABSSWIB.spoof/US9541462/runat_14032006_083243_8686/app_query.fasta_1
-DB=GenBml -QWTF=tatap -SUFFIX=xrge -MINMATCH=0.1 -LOOPFCI=0
-UNITS=bits -START=1 -END=1 -MATRIXX=ol190 -TRANS:human40_cdi -LIST=15
-DOCALIGN=200 -THR SCORE:quality -THR MIN=12 -ALIGN=22 -MODE=LOCAL -OUTFMT=pfo
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abbs06p
-USER=US09-541-462 @CCN 1 1 7415 @runat_14032006_083243_8686 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES 0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=10 -THREADS=1 -XGAP0=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAP0=60 -YGAPEXT=60 -DELEXT=7
```

Database : GenBml:  
1: gb\_bs:  
2: gb\_in:  
3: gb\_env:  
4: gb\_cm:  
5: gb\_or:  
6: gb\_pt:  
7: gb\_ph:  
8: gb\_pr:  
9: gb\_ro:  
10: gb\_sts:  
11: gb\_sy:  
12: gb\_un:  
13: gb\_vl:  
14: gb\_htg:  
15: gb\_dl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	108	100.0	327	8	AF142059		AF142059 Homo sapi
2	108	100.0	433	6	CQ698451		CQ698451 Sequence
3	108	100.0	453	6	CQ690099		CQ690099 Sequence

## ALIGNMENTS

RESULT	1	AF142059	2	LOCUS	Hom sapiens RING finger protein (ROCI)	327 bp	mRNA	PRI 14-JUL-1999
DEFINITION	Homo sapiens	ACCESSION	AF142059	VERSION	GI:4809215	TITLE	ROCI, a homolog of APC11, represents a family of cullin partners with an associated ubiquitin ligase activity	
KEYWORDS		SOURCE	Homo sapiens	ORGANISM	Homo sapiens	JOURNAL	Mol. Cell. 3 (4), 535-541 (1999)	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buttaeostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo	PUBLISHED	10230407	REFERENCE	1 (bases 1 to 327)	
				AUTHORS	Ohta,T., Michel,J.J., Schottelius,A.J. and Xiong,Y.	TITLE	Ohta,T., Michel,J.J., Schottelius,A.J. and Xiong,Y.	
				JOURNAL	University of North Carolina at Chapel Hill, Mason Farm Rd. and Manning Dr., Chapel Hill, NC 27599-7295, USA	FEATURES	Location/Qualifiers	
				Source	1. 327 /organism="Homo sapiens"			



Qy 21 ArgPheGluValLysylTrpAsnAlaValAlaLeutrpAlaTrpAspIleValValAsp 40  
 84 CGCTTCAAGTCATAAGTGGAAATGGATGGCTGGCCCTGGGTGCTGGCATTTGTGGTGT 143

Db 41 AsnCysAlaLileCysArgAsnHisIleMetAspLeucysTrpIleGluCysGlnAlaAsnGln 60  
 144 AACTrGinCCATTGCGAGAACCATATTGATCTTGCATAGAATGTCAGCTAACACG 203

Qy 61 AlaSerAlaThrSerGluGlucysTrpValAlaTrpGlyAlaCysAsnHisAlaPheHis 80  
 204 GCGTCCCCTACTTCAGAGTGTACTGTGCCATGGAGCTGTGTAACAGCTTTCAC 263

Db 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 264 TTCCACTGCACTCTCGTGGTCARAAACAGACAGGTGTCTCCATTGGACAACAGAG 323

Qy 101 TrpGluPheGlnLysylTrpGlyHis 108  
 324 TGGGAATTCAAAAGATGGCCAC 347

Db

RESULT 4  
 Q0695007 LOCUS CQ695007 DEFINITION Sequence 39933 from Patent WO02070737.  
 ACCESSION C0695007 VERSION 1.1 GI:42240530  
 SOURCE Homo sapiens (human)  
 ORGANISM Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 Liew, C.C., Marshall, W.E. and Zhang, H.  
 AUTHORS Liw, C.C., Marshall, W.E. and Zhang, H.  
 TITLE Compositions and methods relating to osteoarthritis  
 DEFINITION Sequence 57254 from Patent WO02070737.  
 ACCESSION CQ712328 VERSION CQ712328.1 GI:42273185  
 KEYWORDS SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 Liew, C.C., Marshall, W.E. and Zhang, H.  
 AUTHORS Liw, C.C., Marshall, W.E. and Zhang, H.  
 TITLE Compositions and methods relating to osteoarthritis  
 DEFINITION Sequence 57254 from Patent WO02070737-A 57254 12-SEP-2002;  
 ACCESSION CQ712328 JOURNAL Chondrogen Inc. (CA)  
 KEYWORDS SOURCE Location/Qualifiers 1 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN Alignment Scores:  
 Pred. No.: 2.4e-112 Length: 471  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservativeness: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) × C0712328 (1-471)

Qy 1 MethionAlaAlaMetAspIleValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
 17 ATGGCGACCGCATGGATGGATAACCCGACGCCACACGCGGGAGTCCTAAACCATGCTTTTCAC 256

Db 21 ArgPheGluValLysylTrpIleValAlaLeutrpAlaTrpAspIleValValAsp 40  
 77 CGCTTGAACTGAAAGTGGAAATGGCAGTAGCCCTCTGGCCTGGATATTGCTTTGAT 136

Qy 21 ArgPheGluValLysylTrpIleValAlaLeutrpAlaTrpAspIleValValAsp 40  
 77 CGCTTGAACTGAAAGTGGAAATGGCAGTAGCCCTCTGGCCTGGATATTGCTTTGAT 136

Db 77 CGCTTGAACTGAAAGTGGAAATGGCAGTAGCCCTCTGGCCTGGATATTGCTTTGAT 136

Qy 41 AsnCysAlaLileCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsnGln 60  
 137 AACTrGCACTCTGGAAACCAATTGATGAGTCAGTACGTAACG 196

Db 61 AlaseralThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 197 GCGTCGCPACTCTGAAAGTGTACTGTGCACTGGGAGTCCTAAACCATGCTTTTCAC 256

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgInvalCysProLeuAspAsnArgGlu 100  
 257 TTCCACTGCACTCTGCTGGCTAAACAGCAAGGTGTGTCATTGGACAACAGAG 316

Db 101 TrpGluPheGlnLysylTrpGlyHis 108  
 317 TGGGAATTCAAAAGATGGCAC 340

Qy 41 AsnCysAlaLileCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsnGln 60  
 140 AACTrGNCATCTGAGAACCATATTGATCTTGCATAGATGCTAGTAACCG 199

Db 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 200 GCGTCGCTACTTCAGAAGTGTACTGTGCACTGGAGTCCTAAACCATGCTTTTCAC 259

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 317 TGGGAATTCAAAAGATGGCAC 340

RESULT 6  
 CQ711142 LOCUS CQ711142 DEFINITION Sequence 56068 from Patent WO02070737.  
 ACCESSION CQ711142 VERSION CQ711142.1 GI:42271999  
 KEYWORDS SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

1 Liew, C.C., Marshall, W.E. and Zhang, H.  
Compositions and methods relating to osteoarthritis  
Patent: WO 02070737 A 56068 12-SEP-2002;  
Chondrogen Inc. (CA)

FEATURES source Location/Qualifiers  
1. .472  
/organism="Homo sapiens"  
/mol type="unassigned DNA"  
/db\_xref="taxon:9606"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 2.41e-112 Length: 472  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x CQ711142 (1-472)

Qy 1 MetAlaAlaAlaAlaMetAspValAspThrProSerGlyYThrAsnSerGlyAlaGlyLysLys 20  
Db 20 ATGGCGGAGGGATGGATGGATAACCCGAGCTGGATAACGGCACAAACGGGGCAAGGAG 79

Qy 21 ArgPheGluVallysLysTPTPAslAlaValAlaLeutPAlaTrpAspIleValAlaAsp 40  
Db 80 CGCTTGAACTGGTAAGGTGAAGAATGGAAATGCAAGTCAGGCCCTGGGATTTGGTGTCAAT 139

Qy 41 AsnCysAlaLeuCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsnGln 60  
Db 140 AACCTGCCATCTCGAGAACCACTATTGGATCTTGATAGATGTAAGCTAACAGAACAG 199

Qy 61 AlaSerAlaThrSerGluGlucYSThrValAlaIlePheGlyIleGluCysAsnHisAlaPheHis 80  
Db 200 GGCCTCCGCTACTCTGAGAGTGTACTGTCGCACTGGAGTCATGGCTTTCAC 259

Qy 81 PheHisCysIleSerArgTPTLeuIlySThrArgGlnValcysProLeuAspIleArgGlu 100  
Db 260 TCCCACTGATCTCTGCTGCTCAAACACGACGGTGTCCATTGGACAACAGAGAG 319

Qy 101 TrpGluPheGlnIlySThrGlyHis 108  
Db 320 TGGGAATCCAAAAGATGGCAC 343

RESULT 8 AX888031

LOCUS AX888031 482 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 3894 from Patent EP1033401.

ACCESSION AX888031

VERSION AX888031.1 GI:40046785

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.  
Sequence tag and encoded human protein  
Patient: JP 200126182-A 3887 02-OCT-2001;

COMMENT OS Homo sapiens (human)  
PN JP 200126182-A/3887

AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.  
TITLE Sequence tag and encoded human protein  
JOURNAL Patient: JP 200126182-A 3887 02-OCT-2001;

GENSET OS Homo sapiens (human)  
PN JP 200126182-A/3887

PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC  
C12N5/10,  
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC  
G06F15/40

CC FH Key  
FEATURES FT CDS Location/Qualifiers  
source Location/Qualifiers  
1. .482  
/organism="Homo sapiens"  
/mol type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 2.45e-112 Length: 482  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x BD027641 (1-482)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyYThrAsnSerGlyAlaGlyLysLys 20  
Db 29 ATGGCGGAGGGATGGATGGATAACCCGAGCTGGATAACGGCACAAACGGGGCAAGGAG 88

Qy 21 ArgPheGluVallysLysTPTPAslAlaValAlaLeutPAlaTrpAspIleValAlaAsp 40  
Db 89 CGTTGAACTGGTAAGGAAAGTGGATGCAAGTCAGTGCCTCTGGCTTGGGATTTGGTGTAT 148

Qy 41 AsnCysAlaLeuCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsnGln 60  
Db 149 AACCTGCCATCTCGAGAACCACTATTGGATCTTGATAGATGTAAGCTAACAGTAACCG 208

Qy 61 AlaSerAlaThrSerGluGlucYSThrValAlaIlePheGlyIleGluCysAsnHisAlaPheHis 80  
Db 209 GGCCTCCGCTACTCTGAGAGTGTACTGTCGCACTGGAGTCATGGCTTTCAC 268

Qy 81 PheHisCysIleSerArgTPTLeuIlySThrArgGlnValcysProLeuAspIleArgGlu 100  
Db 269 TCCACTGATCTCTGCTGCTCAAACACGACGGTGTCCATTGGACACAGAGAG 328

Qy 101 TrpGluPheGlnIlySThrGlyHis 108  
Db 329 TGGGAATCCAAAAGATGGCAC 352

RESULT 8 AX888031

LOCUS AX888031 482 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 3894 from Patent EP1033401.

ACCESSION AX888031

VERSION AX888031.1 GI:40046785

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.  
Expressed sequence tags and encoded human proteins  
Patent: EP 1033401-A 3894 06-SEP-2000;

AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.  
TITLE Express sequence tags and encoded human proteins  
JOURNAL Patent: EP 1033401-A 3894 06-SEP-2000;

GENSET Gense (FR)

FEATURES Location/Qualifiers  
1. .482  
/organism="Homo sapiens"  
/mol type="unassigned DNA"  
/db\_xref="taxon:9606"  
29. .355  
/note="unnamed protein product"  
/codon\_start=1



Query Match: 100.0%  
DB: 6 Indels: 0 Gaps: 0

Alignment Scores:  
Pred. No.: 2.55e-112 Length: 504  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x AR640605 (1-504)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyYalaglyLyslys 20  
Db 18 ATGGCGCCGCGATGGATACCCGCCAGCGAACAAACGGGGCAAGAG 77

Qy 21 ArgPheGluVallysLysTrpAsnAlaValAlaLeuTrpAlaLeuTrpAspIleValValAsp 40  
Db 78 CGCTTGAACTTAAAGTGAATCAGGGCCCTTCGGCCTGGAAATTGGCTGTAT 137

Qy 41 AsnCysAlaIleCysArgSerHisIleMetAspLeuCysIleGluCysGlnAlaAsnAln 60  
Db 138 AACATGGCCATCTGGAGAACCATTTGATGATCTTGATGATGTCAGGCCAACAG 197

Qy 61 AlaserAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
Db 198 GCGTCAGTACTTCGAAAGTGTACGGTGCATGGGAAGTCTCAACCATGCTTTCAT 257

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
Db 258 TTCCACTGATCTCTCGATGCTCAAACAGGGAGGTGTGCCAGAACAGAG 317

Qy 101 TrpGluIleGlnLysTrpGlyHis 108  
Db 318 TGGGAGTCCAGAAGTAGTGGCAT 341

RESULT 1.1  
AF:40599 LOCUS AF140599 504 bp mRNA linear ROD 11-MAY-1999  
DEFINITION Mus musculus ring-box protein 1 (Rbx1) mRNA, complete cds.  
ACCESSION AF140599  
VERSION AF140599.1 GI:4769005  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE Kamura,T., Conrad,M.N., Skowyra,D., Moreland,R.J.,  
Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Eledge,S.J.,  
Conaway,R.C., Harper,J.W. and Conaway,J.W.  
TITLE Rbx1, a component of the VHL tumor suppressor complex and SCP  
ubiquitin ligase  
SCIENCE 284 (5414), 657-661 (1999)  
JOURNAL JOURNAL OF BIOLOGICAL CHEMISTRY 274 (5414), 34444-34451 (1999)  
PUBLMED 10213691  
REFERENCE 2 (bases 1 to 504)  
AUTHORS Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.  
TITLE Direct Submission  
JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma  
Med. Res. Fdn., 825 NE 13th St., Oklahoma City, OK 73104, USA  
FEATURES Location/Qualifiers  
source 1..504  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
gene 1..504  
/gene="rbx1"  
CDS 18..344  
/gene="rbx1"  
/note="component of VHL tumor suppressor complex and SCF  
ubiquitin ligase"  
/codon\_start=1  
/product="ring-box protein 1"  
/protein\_id="P429716.1"  
/db\_xref="GI:469006"  
/translation="MAAAMDVDPSGTNSGAGKRFEVKNNAVALAWDIDVNDNCAI  
CRNHIMDLICIEQANQASATSEECTVAVGVCNHAHFHCISRMKTRQVCLDNRNEW  
FQKIGH"  
ORIGIN

Db 7 ATGGGCCAGGGATGGATGCGATACCCCGACGGCCCAACAGGGCGGGCAAGGAG 66  
 Qy 21 ArgPheGluValLysIleSTPAsnAlaValAlaLeuTPAlaTPAspIleValAsp 40  
 Db 67 CGCTTGAAGTAAAGTGGATGCGCTTCGGCTGGATATGTGGTTGAT 126  
 Qy 41 AsnCysAlaLysCysArgAsnIleMetAspLeuCysIleGlucySGinAlaAsnGln 60  
 Db 127 AACTGTGCCATTCTGAGAACCATATGGATCTTGCAATAAGTAACACAG 186  
 Qy 61 AlaSerAlaThrSerGluGlucySthrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 187 GCGTCCCTACTTCAGAGAGTGTACTGTCGATGGAGACTGTCGTAACCATGCRITTCAC 246  
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 247 TTCCACTGCATCTCCCTGCGTCAAAACGACGGTGISTCCATTGGCAACAGAGAG 306  
 Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 307 TGGGAATTCAAAAGTATGGGAC 330

RESULT 13  
 BD271520 LOCUS VonHippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase. PAT 17-JUL-2003  
 DEFINITION VonHippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase.

ACCESSION BD271520  
 VERSION GI:33081288  
 KEYWORDS JP 2002-41775-A/1.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 508)  
 CONAWAY,J.W., CONAWAY,R.C. and KAMURA,T.  
 VonHippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase  
 Patent: JP 2002541775-A 1 10-DEC-2002;  
 OKLAHOMA MEDICAL RESEARCH FOUNDATION  
 OS Homo sapiens (human)  
 PN JP 2002541775-A/1  
 PD 10-DEC-2002  
 PF 25-FEB-2000 JP 2000601023  
 PR 26-FEB-1999 US 601211787  
 PI JOHN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA, PC  
 C12N15/09, A61K38/00, A61K45/00, A61P35/00, C07K14/47, PC  
 PC  
 FT source 1..508 /organism='Homo sapiens (human)'  
 FT Location/Qualifiers 1..508  
 source GO1N33/68 /organism="Homo sapiens"  
 CC vonHippel-Lindau tumor suppressor complex and novel component  
 CC of SCF  
 CC ubiquitin ligase  
 FH Key Location/Qualifiers 1..508  
 FT source 1..508 /organism='Homo sapiens (human)'  
 FEATURES source 1..508 /organism="Homo sapiens"  
 /mol\_type="Genomic DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN Alignment Scores:  
 Pred. No.: 2.57e-112 Length: 508  
 Score: 508 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x BD271520 (1-508)  
 Qy 1 MetAlaAlaAlaMetAspIleValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
 Db 7 ATGGCGCAGCGATGGATGCGCTTCGGCTGGATACCCGGCCACAGGGCGCAGAAG 66  
 Qy 21 ArgPheGluValLysIleSTPAsnAlaValAlaLeuTPAlaTPAspIleValAsp 40  
 Db 67 CGCTTGAAGTAAAGTGGATGCGCTTCGGCTGGATATGTGGTTGAT 126  
 Qy 41 AsnCysAlaLysCysArgAsnIleMetAspLeuCysIleGlucySGinAlaAsnGln 60  
 Db 127 AACRTGTGCCATTCTGAGAACCATATGGATCTTGCAATAAGTGTGGATATGTGGTTGAT 186  
 Qy 61 AlaSerAlaThrSerGluGlucySthrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 187 GCGTCCCTACTTCAGAGAGTGTACTGTCGATGGAGACTGTCGTAACCATGCTTCAC 246  
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 247 TTCCACTGCATCTCCCTGCGTCAAAACGACGGTGISTCCATTGGCAACAGAGAG 306  
 Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 307 TGGGAATTCAAAAGTATGGGAC 330

RESULT 14  
 AR640603 LOCUS AR640603 Sequence 3 from patent US 6858709.  
 DEFINITION AR640603 AR640603 Accession AR640603.1 GI:62775412  
 VERSION AR640603.1  
 KEYWORDS Unknown.  
 SOURCE Unclassified.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 508)  
 AUTHORS CONAWAY,J.W., CONAWAY,R.C. and KAMURA,T.  
 TITLE Component of von Hippel-Lindau tumor suppressor complex and SCF ubiquitin ligase  
 JOURNAL Patent: US 6858709-A 3 22-FEB-2005;  
 Oklahoma Medical Research Foundation; Oklahoma City, OK  
 FEATURES Location/Qualifiers 1..508  
 SOURCE /organism="unknown"  
 /mol\_type="genomic DNA"  
 ORIGIN Alignment Scores:  
 Pred. No.: 2.57e-112 Length: 508  
 Score: 508 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x AR640603 (1-508)  
 Qy 1 MetAlaAlaAlaMetAspIleValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
 Db 7 ATGGCGCAGCGATGGATCTGGCTTCGGATACCCGGCACCAAGGGCGCAGAAG 66  
 Qy 21 ArgPheGluValLysIleSTPAsnAlaValAlaLeuTPAlaTPAspIleValAsp 40  
 Db 67 CGCTTGAAGTAAAGTGGATGCGCTTCGGCTGGATATGTGGTTGAT 126  
 Qy 41 AsnCysAlaLysCysArgAsnIleMetAspLeuCysIleGlucySGinAlaAsnGln 60  
 Db 127 AACRTGTGCCATTCTGAGAACCATATGGATCTTGCAATAAGTGTGGATATGTGGTTGAT 186  
 Qy 61 AlaSerAlaThrSerGluGlucySthrValAlaTrpGlyValCysAsnHisAlaPheHis 80

Qy	187	GCTCCGGTACTTCAGAAGATGTTGATGGGAGTCAGTGTAACTATGGTTTCAC	246	4.1 AsnCysAlaIleCysSerAsnHisIleMetAspLeuTrpAspIleGluCysGlnAlaAsnGln 60
Db	81	PhenylCysIleSerArgTripleUlySthrArgInValCysProLeuAspAsnArgGlu	100	127 AACTGTGCCATTGAGAACCACTATGGAACTTGATGATGATGTTTCAC 186
Qy	247	TTCACCGCATCTCTCGTGTCAAACACGACAGGTGTGTCATGACAACAGAGAG	306	61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysSerAsnHisIlaPheHis 80
Db	101	TrpGluPheGlnLysTrpGlyHis	108	187 GCTCCGGTACTTCAGAAGATGTTGATGATGTTTCAC 246
Qy	307	TGGAAATTCCAAGATGGGCAC	330	81 PheHisCysIleSerArgTripleUlySthrArgGlnValCysProLeuAspAsnArgGlu 100
Db	RESULT 15			247 TTCCACTGATCTCGCTGTCAAACACGACAGGTGTGTCATGACAACAGAGAG 306
AF140598	AF140598	508 bp mRNA Homo Sapiens ring-box protein 1 (RBX1) mRNA, complete cds.	PRI 11-MAY-1999	Qy 101 TrpGluPheGlnLysTrpGlyHis 108
LOCUS	AF140598			Db 307 TGGAAATTCCAAGATGGGCAC 330
DEFINITION				
VERSION	AF140598.1			
KEYWORDS				
SOURCE		Homo sapiens (human)		RESULT 16
ORGANISM		Homo sapiens		CQ701366
		Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;		LOCUS CQ701366 523 bp DNA
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		DEFINITION Sequence 46292 from Patent WO02070737.
		Hominidae; Homo.		ACCESSION CQ701366
		1 (bases 1 to 508)		VERSION CQ701366.1 GI:42262133
REFERENCE	AUTHORS	Kamura, T., Koepf, D.M., Conrad, M.N., Skowron, D., Moreland, R.J., Ilissopoulos, O., Lane, W.S., Kaelin, W.G. Jr., Elledge, S.J., Conaway, R.C., Harper, J.W., and Conaway, J.W.,		KEYWORDS Homo sapiens (human)
	TITLE	Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase		ORGANISM Homo sapiens
JOURNAL	PUBLISHED	Science 284 (5114), 657-661 (1999)		Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
	2 (bases 1 to 508)	10213691		
AUTHORS	TITLE	Kamura, T., Lans, W.S., Conaway, R.C. and Conaway, J.W.		REFERENCE 1
JOURNAL	PUBLISHED	Direct Submission		AUTHORS Lieu, C.C., Marshall, M.E. and Zhang, H.
FEATURES		Submitted (05-APR-1999) Prog. Molec. Cell. Biol., HHMI, Oklahoma Med. Res. Fdn., 825 NE 13th St., Oklahoma City, OK 73104, USA		TITLE Compositions and methods relating to osteoarthritis Patent: WO 02070737-A 4622 12-SEP-2002; Chondrogen Inc. (CA)
source		Location/Qualifiers 1..508		FEATURES Location/Qualifiers source
gene		/organism="Homo sapiens"		ORIGIN
CDS		/mol type="mRNA"		Alignment Scores:
		/db_xref="taxon:9606"		Pred. No.: 2.64e-112 Length: 523
		1..508		Score: 108.00 Matches: 108
		/gene= "RBX1"		Percent Similarity: 100.0%
		7..333		Best Local Similarity: 100.0%
		/gene= "RBX1"		Query Match: 100.0%
				DB: 6
				US-09-541-462B-2 (1-108) x CQ701366 (1-523)
Qy				Qy 1 MetalAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20
Db				Db 79 CGCTTGAAGTGAAGTGAATCTGGCTCTGGATAGCTGAAATATGTTGTTGAT 138
Qy				Qy 41 AsnCysAlaIleCysArgSerGlnAlaAsnGln 60
Db				Db 139 AACCTGCACTCTGGAAACCACTATGATCTGGATAGATGAAATGTCAGCTTAC 198
Qy				Qy 61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysSerAsnHisIlaPheHis 80
Db				Db 199 GCGTCGGTACTTCAGAAGGTACTGTCATGGGACCATGCTAACATGCTTCAC 258
Qy				Qy 81 PheHisCysIleSerArgTripleUlySthrArgInValCysProLeuAspAsnArgGlu 100
Db				Db 259 TTCCACTGCACTCTGGCTGCTAACACGACAGGTGTGTCATGGACAAACAGAGAG 318
Qy				Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db				Db 319 TGGCAATTCCAAAAGATGTCGGSCAC 342
Qy	1	MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20		
Db	7	ATGGCGGCKACGATGGATGGATACCCGACCAACGGCCGGAGAG 66		
Qy	21	ArgPheGluValLysLysTrpAlaValAlaLeuTrpAlaTrpAspIleValAsp 40		
Db	67	CGCTTGTGAACTGAAAAAGTCGAATGCTGCTGCTGCTAACACGACAGAGAG 126		



	Alignment Scores:	2.69e-112
Proc. No.:	1	MetAlaAlaAlaLavetAspValAspThrProSerGlyThrAsnSerGlyYalaGlyLysLys
Score:	108.00	Length: 535 Matches: 108 Conservative: 0 Percent Similarity: 100.0% Best Local Similarity: 100.0% Query Match: 100.0% De: 0 Gaps: 0
REMARK	US-09-541-462B-2 (1-108) x BC001466 (1-535)	
JOURNAL	QY	1 MetAlaAlaAlaLavetAspValAspThrProSerGlyThrAsnSerGlyYalaGlyLysLys
PUBLISHED	Db	2 6 ArgGGGAGGGATGGATGGATGTGATAACCCGAGGGCCAACGGGGCGGCAAGAGAG 65
AUTHORS	Db	21 ArgPheGluValLysLystrpAsnAlaLeuTrpAlaTrpAspIleValValAsp 40
COMMENT	Db	21 6 CGCTTGAAGTGAAGAAACTGGATGCACTGGCCTCTGGCTTGGATATTGTTGAT 125
NIH MGC Project	Db	21 66 AlaSerAlaThrSerGluLysThrValAlaTrpGlyValCysSashisAlaPheHis 80
Direct Submission	Db	21 66 GCGCCGFACTGAGAGTGACTTGAGAAGTGACTGCGATGGAGTCTTAACATGCTTTGAC 245
Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20832-2550, USA	QY	41 AsnCysAlaLilecysArgAsnHiSlMetAspLeuCysGlnAlaAsnGln 60
NIH-MGC Project URL: http://mcg.nci.nih.gov	Db	41 126 AACTGTGCCATCGAGAACCATPATGGATCTTCATAGATGTCAAGCTAACAG 185
On Sep 16, 2003 this sequence version replaced gi:12655214.	Db	41 On Sep 16, 2003 this sequence version replaced gi:12655214.
Contact: MGC help desk	QY	61 AlaSerAlaThrSerGluLysThrValAlaTrpGlyValCysSashisAlaPheHis 80
Email: cgbbs-fomail.nih.gov	Db	61 186 GCGCCGFACTGAGAGTGACTTGAGAAGTGACTGCGATGGAGTCTTAACATGCTTTGAC 245
Tissue Procurement: ATCC	Db	61 186 GCGCCGFACTGAGAGTGACTTGAGAAGTGACTGCGATGGAGTCTTAACATGCTTTGAC 245
CNA Library Preparation: Rubin Laboratory	QY	81 PheHisCysIleSerArgTrpLeuLysThrArgInValCysProLeuAspBarGlu 100
CNA Library Arrayed by: The I.M.A.G.E. Consortium (L1NL)	Db	81 246 TTCGACTGCGATCTCGCTGGCTAAAACGACAGGTGTCCATTGGACAACZAGAGG 305
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland	QY	81 RESULT 19
Web site: http://www.nisc.nih.gov/	Db	81 CR456560 LOCUS CR456560 mRNA linear PRI 13-JAN-2001 CDNA clone C22ORF:pGEM.REX1.
Contact: nisc@nigri.nih.gov	Db	81 DEFINITION Homo sapiens RBX1 full length open reading frame (ORF) CDNA clone C22ORF:pGEM.REX1.
Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghichi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Mastriani, B., Mastriani, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stancaripop, S., Thomas, P.J., Touchman, J.W., Tsurugon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.	Db	81 ACCESSION CR456560.1 GI:47678650
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/L1NL at: http://image.l1nl.gov	Db	81 VERSION CR456560 CDNA; chromosome 22; ORF.
Series: IRAL Plate: 4 Row: j Column: 15.	Db	81 SOURCE Homo sapiens
Location/Qualifiers 1..535	Db	81 ORGANISM Homo sapiens
/organism="Homo sapiens"	Db	81 LOCATION
/mol type="mRNA"	Db	81 JOURNAL Genome Biol. 5 (10), R84 (2004)
/db_xref="taxon:9606"	Db	81 PUBLMED 15461802
/clone="MGC:1481 IMAGE:3138751"	Db	81 REFERENCE 2 (bases 1 to 535)
/tissue type="Placenta; choriocarcinoma"	Db	81 AUTHORS Collins,J.E., Wright,C.L., Edwards,C.A., Davis,M.P., Grinham,J.A., Cole,C.G., Goward,M.E., Aguado,B., Mallya,M., Mokrab,Y.,, Huckle,E.J., Beere,D.M. and Dunham,I.
/clone_id="NIH_MGC_21"	Db	81 TITLE A genome annotation-driven approach to cloning the human ORFeome
/lab_host="DH10B-R"	Db	81 JOURNAL Genome Biol. 5 (10), R84 (2004)
/note="vector: pOTB7"	Db	81 COMMENT Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: c22@sanger.ac.uk Manuscript Sanger Institute name : pGEM RBX1 Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see http://www.sanger.ac.uk/HGP/Chr22/.
gene	Db	81 FEATURES 1. .535
source	Db	81 /gene="RBX1"
	Db	81 /note="Synonyms: ROC1, RNF75, BA554C12.1, MGC13357."
	Db	81 /product="MGC1481"
	Db	81 /db_xref="GeneID:603814"
	Db	81 /db_xref="MM:603814"
	Db	81 /db_xref="GeneID:9978"
	Db	81 /db_xref="GeneID:9978"
	Db	81 /translation="MMAAMDDVDTPSGTNSGGAKKRFEVKNNAVALWADLVVDNCATCRNHMDUCIECOANQASATSECTVANGVCHAFHFACISRLKTRQVCPLDNREWEFQYGH"
CDS	Db	81 /mol_type="mRNA"
	Db	81 /db_xref="taxon:9606"
	Db	81 /ch_xref="taxon:122"

/clone="pGEM.RBX1"  
 /lab\_host="JM109"  
 1..535  
 19..345  
 /gene="RBX1"  
 /gene="RBX1"  
 /codon\_start=1  
 /protein\_id="CAG30446\_1"  
 /db\_xref="GO:47678651"  
 /db\_xref="InterPro:IPR001841"  
 /db\_xref="UniProt:SWISS-Prot:P62877"  
 /translation="MAAMMDVDTPECTNSAGKKRFEVKRNAAVALWANDIVDNCAI  
 CRNHNIDLICEQANQASATSEECTVANGCNHAFHFCISRWLKTRQVCLDNRWE  
 FQKYGI"

**ORIGIN**

Pred. No.:	Alignment Scores:	Length:	Matches:	Conservative:	REMARK	JOURNAL	REFERENCE
Score:	2.69e-112	535	108	0			Strausberg, R.
Percent Similarity:	100.0%			0			
Best Local Similarity:	100.0%			0			
Query Match:				0			
DB:				0			

US-09-541-462B-2 (1-108) x CR456560 (1-535)

Qy	1 MetAlaAlaAlaMetAlaAlaMetAlaAlaAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db	19 ArgGGGAGCCATGGGTGATAACCCGAGGGCCAAGNGGCCGCGGCAAGAAG 78
Qy	21 ArgPheGluValLysLisSTPAsnAlaValAlaLeuTPalatTPaspIleValAsp 40
Db	79 CGCTTTCGAGTGRAANGTGGATGGCTCTGGCTTGGAATATGGTGTGTGAT 138
Qy	41 AsnCysAlaIleCysArgAsnIleMetAspLeucysIleGlucysGlnAlaAsnGln 60
Db	139 AACTGTGCCATCTGAGAAACCACATATGGATCTTGCATAGATGCTANCACAG 198
Qy	61 AlaSerIleIleSerGluGlucysThrValAlaIleTrpGlyValCysSerHisAlaPheHis 80
Db	199 GCTCCGGTACTCTGAGAGTGACTGCTGATGGAGTGCTGTAACCATGCTTTAC 258
Qy	81 PheHisCysIleSerArgTgIleUlySthrArgGlnValCysProLeuAspAsnArgGlu 100
Db	259 TTCCACTGCATCTCCCTGGCTCAAACGACAGGTGTGCCATTGGACAACAGAG 318
Qy	101 TrpGluIleGlnIleStryGlyHis 108
Db	319 TGGAAATTCCAAAAGATGGCAC 342

REFERENCE AUTHORS

LOCUS BC017370 554 bp mRNA linear PRI 21-OCT-2003 CDS

DEFINITION Homo sapiens ring-box 1, mRNA (cDNA clone IMAGE:4065797), partial CDS

KEYWORDS

ORGANISM Homo sapiens

ACCESSION BC017370\_1 GI:16924201

VERSION BC017370

KEYWORDS

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 554)

REFERENCE AUTHORS

STRASBERG, R.L., PEINGOLD, E.A., GROUSE, L.H., DERGE, J.G., KLAUSNER, R.D., COLLINS, F.S., WAGNER, L., SHENMEN, C.M., SCHULER, G.D., ALTSCHUL, S.F., ZEEBERG, B., BUETOW, K.H., SCHAEFER, C.F., BHAT, N.K., HOPKINS, R.F., JORDAN, H., MOORE, T., MAX, S.I., WANG, J., HSIEH, F., DIATCHENKO, L., MARUSINA, K., FARMER, A.A., RUBIN, G.M., HONG, L., SCHAFFER, M., SOARES, M.B., BONALDO, M.P., CASAVANT, T.L., SCHEETZ, T.E., BROWNSTEIN, M.J., USDIN, T.B., TOSHIYUKI, S., CARNINCI, P., PRANGE, C., RAHA, S., LOQUELLANO, N.A., PETERS, G.J.,

REFERENCE AUTHORS

MULLAHY, S.J., BOSAK, S.A., MCBWAN, P.J., MCKERNAN, K.J., MAIEK, J.A., GUNARATNE, P.H., RICHARDS, S., WORLEY, K.C., HAILE, S., GARCIA, A.M., GAY, L.J., HUIYK, S.W., VILLALON, D.K., MURNY, D.M., SODERGREN, B.J., LU, X., GIBBS, R.A., FAHEY, J., HELTON, E., KETTERMAN, M., MADAN, A., RODRIGUES, S., SANCHEZ, A., WHITING, M., MADAN, A., YOUNG, A.C., RODRIGUES, S., BOUFFARD, G.G., BLAKESLEY, R.W., TOUCHMAN, J.W., GREEN, E.D., DICKSON, M.C., RODRIGUEZ, A., GRIMWOOD, J., SCHMUTZ, J., MYERS, R.M., BUTTERFIELD, Y.S., KRZYWINSKI, M.I., SKALSKA, U., SMAILUS, D.E., SCHNERCH, A., SCHEIN, J.E., JONES, S.J., AND MARRA, M.A., TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932 (bases 1 to 554)

AUTHORS STRASBERG, R.

TITLE Direct Submission

JOURNAL Submitted (13-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC). Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Tissue Procurement: ATCC

CDSNA Library Arrayed by: CLONTECH Laboratories, Inc.

CDSNA Library Prepared by: The I.M.A.G.E. Consortium (LNL)

CDSNA Sequencing by: Institute for Systems Biology

http://www.systemsbio.org

contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahey, Brin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov

Series: IRAP Plate: 19 Row: C Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22091459.

Location/Qualifiers

FEATURES

Source

1..554

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4065797"  
 /tissue="Brain, glioblastoma"  
 /clone\_id="NTM MGC\_57"  
 /lab\_host="DH10B"  
 /note="vector: pDNR-LIB"  
 <1..554  
 /gene="RBX1"  
 /note="synonyms: ROC1, B554C12.1, MGC133357, MGC1481, RNFL5"  
 /db\_xref="GeneID:9978"  
 /db\_xref="MIN:603814"  
 <1..349  
 /gene="RBX1"  
 /codon\_start=2  
 /product="RBX1 protein"  
 /protein\_id="AAH1370.2"  
 /db\_xref="GI:32425477"  
 /ab\_xref="GeneID:9978"  
 /db\_xref="MIM:603814"  
 /translaton="GRPCVKNAAMDVDTPSGTNSAGIKKRFEVKVNNAVALWAWDI  
 LDNRCNAICRNHINDLCIQCQANQASATSECTVAWGVNCNHAHFHCISRWLKTRQVC  
 CP 80..346  
 /gene="RBX1"  
 /note="APC11; Region: COG5184, APC11, Component of SCF ubiquitin ligase and anaphase-promoting complex [Positratnional modification, protein turnover, chaperones / Cell division and chromosome partitioning]"  
 /db\_xref="CDD:COG5194"

misc\_feature

ORIGIN



Search completed: March 15, 2006, 10:14:57  
Job time : 2491 secs

This Page Blank (uspto)



GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 4940  
; LENGTH: 507  
; TYPE: DNA  
; ORGANISM: Human  
; SEQ ID NO: US-09-949-016-4940

Alignment Scores:  
Pred. No.: 1 MetAlaAlaAlaAlaValAspValAspThrProSerGlyIleArgLysLys 20  
Score: 108 00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 100.0%  
DB: 3 Gabs: 0

US-09-541-462B-2 (1-108) x US-09-949-016-4940 (1-507)

QY 1 MetAlaAlaAlaAlaValAspValAspThrProSerGlyIleArgLysLys 20  
Db 7 ATGGGGAGCGATGGATGGATACCCGAGGCCAACAGGGGAGGGAGAGAG 66

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
Db 67 CGCTTGAAAGTAGGAATTCAGTAGCCTCTGGCTTGTGGATTATGGTTGAT 126

QY 41 AsnCysAlaIleCysArgAsnHiSileLeuAspIeuCysClnAlaAsnGln 60  
Db 127 AACGTGCCCCATCTCAGGACCACATTGGATCTTGCATAGATGTCAGCTAACAG 186

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHiAlaPheHis 80  
Db 187 GCGCCGGTACTTCAGAGCTGACTGCGAAGGGAGTCCTTAACCATGCTTTTCAC 246

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgInvalCysProLeuAspAsnArgGlu 100  
Db 247 TTCACTGATCTCAGGCTTCAGGAACTATGGCTATTGACAACAGAGAG 306

QY 101 TrpGluPheGlnLysLysTrpGlyHis 108  
Db 307 TGGGAAATTCCAAAAGACTATGGCAC 330

RESULT 4  
US-09-914-324A-3  
; Sequence 3, Application US/09914324A  
; GENERAL INFORMATION:  
; APPLICANT: Conaway, Joan A.  
; APPLICANT: Kamura, Takumi  
; APPLICANT: Okanoma Medical Research Foundation  
; TITLE OF INVENTION: von Hippel-Lindau Tumor Suppressor  
; FILE REFERENCE: 021044-004600US  
; CURRENT APPLICATION NUMBER: US/09/914,324A  
; CURRENT FILING DATE: 2003-02-11  
; PRIOR APPLICATION NUMBER: US 60/121,787  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 5  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE: CDS  
; NAME/KEY: CDS  
; LOCATION: (18)..(344)  
; OTHER INFORMATION: Rbx1  
; SEQ ID NO: US-09-914-324A-5

Alignment Scores:  
Pred. No.: 1.42e-109  
Score: 108.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 100.0%  
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-914-324A-5 (1-504)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyIleArgLysLys 20  
Db 18 ATGGCGCGGGATGGATACCCCGGGCAACAGGGGCAAGAG 77

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
Db 78 CGCTTGAAAGTAGGAATGGAGTCGCTCTGGACATTTGTCGTTGAT 137

QY 41 AsnCysAlaIleCysArgAsnHiSileLeuAspIeuCysClnAlaAsnGln 60  
Db 138 AACTGTGCCATCTGAGAACACATAATGATGTAGCCAAACXAG 197

QY 61 AlaSerAlaThrSerGluCysThrValAlaIleTrpGlyValCysAsnHiAlaPheHis 80  
Db 198 GGTCAGTCAATTCCAAGACTGAGTGTAGCTGGCTTCAGGAAACAGAG 257

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgInvalCysProLeuAspAsnArgGlu 100  
Db 258 TTCCACTGATCTCAGTGGCTCAAAGGGCACTGTCGAAACATGCTTTTCAT 317

QY 101 TrpGluPheGlnLysLysTrpGlyHis 108  
Db 318 TGGGAAATTCCAAAAGATGGCCAT 341

RESULT 3  
US-09-949-016-4940  
; Sequence 4940, Application US/09949016  
; Patent No. 6812339

```

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1
US-09-914-324A-3

Alignment Scores:
Pred. No.: 1.43e-109 Length: 508
Score: 84.00 Matches: 84
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 77.8% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)

Qy 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaIle 44
Db 2770 AAAAAATGAAATCAGTAGCCCTCTGGCCCTGGGATATTGTGGTGAATCTGTGCAC 2829

Qy 45 CyBarGAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64
Db 2830 TGAGGAAACCAATTATGATCTTGATAGANTGCAAGCTAACAGCGTGGCTACT 2889

Qy 65 SerGluGluCysIleSerAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIle 84
Db 2890 TCAGAAAGTGTACTGTGCATGGGACTCTGAACATGCRTTCACTGCCACTGCATC 2949

Qy 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAsnArgGluTrpGluPheGln 104
Db 2950 TCTGCGTCGGCTAAACACGACAGGTGTGTCATGGACAACAGAGTGGAAATTCCA 3009

Qy 1 MetAlaIalaAlaMetAspValAlaSerPheProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 7 ATGGCGCACGGCATGGATGATGCGATACCCGACCAAGCGCCGGCAAGAG 66

Qy 21 ArgPheGluValIleLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40
Db 67 CGCTTGAAGTAAAAGTGGATGCAAGTAGCCTGGCTGGATATGGTTGAT 126

Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 127 ACTGTGCCATCTGCAGAACACCATATTGGATCTTGCATAAGAACTCAAGCTAACAG 186

Qy 61 AlAsnAlaIleSerGluGluCysIleSerAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 187 GGTTCCGCTACTTCAGAGGTGTACTGCTGATGGGAGCTGTAAACGCTTTCAC 246

Qy 81 PheHisCysIleSerArgTripeulySerArgGlnValCysProLeuAspAsnArgGlu 100
Db 247 TTCCACTGCACTCTCGCTGGCTCAAACACGACAGTGGCACACAGAG 306

Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 307 TGGGAAATCCAAAAGATGGCAC 330

RESULT 5
US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. 6509456
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Human Proteases and Polynucleotides Encoding the Same
CURRENT APPLICATION NUMBER: US/10/214-811
PRIORITY NUMBER: US/09/780, 016
CURRENT FILING DATE: 2002-08-07
PRIORITY FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 27
LENGTH: 3208
TYPE: DNA
ORGANISM: Homo sapiens
US-09-541-462B-2 (1-108) x US-10-214-811-27 (1-3208)

Alignment Scores:
Pred. No.: 1.71e-82 Length: 3208
Score: 84.00 Matches: 84
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 77.8% Indels: 0
DB: 3 Gaps: 0

Qy 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaIle 44
Db 2770 AAAAAATGAAATCAGTAGCCCTCTGGCCCTGGGATATTGTGGTGAATCTGTGCAC 2829

```

Qy 45 CysArgAsnHistileMetAspLeuCysIleGluCysGlnAlaSerAlaSerAlaThr 64  
Db 2830 TGCGGAACCATATGATCTTGATAAGTCAAGTAAACAGCGGCCATC 2889

Qy 65 SerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisHeisCysIle 84  
Db 2890 TCAGAAGGTACTGTCGATGCCATGGATCTGTAACCATGCTTCACCTCCACTGCATC 2949

Qy 85 SerArgTrpIleLysThrArgInValCysProLeuAsnArgGluTrpGluPheGln 104  
Db 2950 TCTCGCTGGCTCAAACACAGGTGTCATTGGAACTGGAACTGGGAAATTCCA 3009

Qy 105 LysTrpGlyHis 108  
Db 3010 AAGTAGGGCAC 3021

---

RESULT 7  
; Sequence 27 Application US/10766074  
; Patent No. 6881563

; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6881563 eel Human Proteases and  
; FILE REFERENCE: LEX-0132-USA  
; CURRENT APPLICATION NUMBER: US/10/766, 074  
; CURRENT FILING DATE: 2004-01-28  
; PRIORITY NUMBER: US/10/214, 811  
; PRIORITY FILING DATE: 2002-08-07  
; PRIORITY APPLICATION NUMBER: US/09/780, 016  
; PRIORITY FILING DATE: 2001-02-09  
; PRIORITY APPLICATION NUMBER: US 60/181, 294  
; PRIORITY FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 27  
; LENGTH: 3208  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; US-10-766-074-27

Alignment Scores:  
Pred. No.: 1.71e-82 Length: 3208  
Score: 84.00 Matches: 84  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Missmatches: 0  
Query Match: 77.8% Indels: 0  
DB: 3  
US-10-766-074-27 (1-3208)

Qy 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsnCysAlaIle 44  
Db 2770 AAAAATGGATTGAGTAGCCCTCTGGCTGGATATTGGTTGATATTGCCATT 2829

Qy 45 CysArgAsnHistileMetAspLeuCysIleGluCysGlnAlaSerAlaThr 64  
Db 2830 TGCGGAACCATATGATCTTGATAAGTCAAGTAAACAGCGGCCATC 2889

Qy 65 SerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisHeisCysIle 84  
Db 2890 TCAGAAGGTACTGTCGATGCCATGGATCTGTAACCATGCTTCACCTCCACTGCATC 2949

Qy 85 SerArgTrpIleLysThrArgInValCysProLeuAsnArgGluTrpGluPheGln 104  
Db 2950 TCTCGCTGGCTCAAACACAGCACAGGTGTCATTGGAACTGGGAAATTCCA 3009

---

Qy 105 LysTrpGlyHis 108  
Db 3010 AAGTAGGGCAC 3021

RESULT 8  
; Sequence 1731, Application US/09640211A  
; Patent No. 683346  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; Modification of Gene Transcription  
; FILE REFERENCE: 11000.1041CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 1731  
; LENGTH: 411  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
; FEATURE:  
; NAME KEY: misc feature  
; LOCATION: (1)..(411)  
; OTHER INFORMATION: n = A,T,C or G  
; US-09-640-211A-1731

Alignment Scores:  
Pred. No.: 2.49e-72 Length: 411  
Score: 74.00 Matches: 74  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Missmatches: 0  
Query Match: 68.5% Indels: 0  
DB: 3  
US-09-640-211A-1731 (1-411)

Qy 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsnCysAlaIle 44  
Db 176 AAGAAGTGGATGGTGTAGCCCTTGCGCTGGATATTGGTTGATATTGCCATT 2355

Qy 45 CysArgAsnHistileMetAspLeuCysIleGluCysGlnAlaSerAlaThr 64  
Db 236 TGCGAAGAACCATATGACCTCTGTGATTGAGTGTAGCCATTCAAGAAGTGCACA 295

Qy 65 SerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisHeisCysIle 84  
Db 296 AGTGGAGAATGCTATGGTGGATGGGGTGTGATTCATCCCTTCATTGCCATT 355

Qy 85 SerArgTrpIleLysThrArgInValCysProLeuAsnArg 98  
Db 356 AGTCGGTGGCTCAAACACAGCACAGCAAGTCTGCCATTAGATAAT 397

RESULT 9  
; Sequence 10371, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J. B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J. Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59 US2. REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIORITY APPLICATION NUMBER: US 60/1122, 487  
; PRIORITY FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent .pm

```

: SEQ ID NO 10371
: LENGTH: 402
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: misc_feature
: NAME/KEY: misc_feature
: LOCATION: 20
: OTHER INFORMATION: k=g or t
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 38
: OTHER INFORMATION: s=g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 79
: OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-10371

Alignment Scores:
Pred. No.: 1.76e-51 Length: 402
Score: 55.00 Matches: 55
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 50.9% Indexes: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-513-999C-10371 (1-402)
Qy 54 IleGluCysGlnAlaSerGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
Db 108 ATAGAATGTCAGCTAACCGTGGTACTCTGAAAGGTGACTGTGCATGGGA 167

RESULT 10
Qy 74 ValCysSerHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
Db 168 GTCTGPAACCATGCTTCACTGCCATCTGCTGGCTAAACACGACAGGTG 227

Qy 94 CysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGlyHis 108
Db 228 TGTCATTGGACAACAGAGTGGAATTCCAAAAGATGGCAC 272

RESULT 10
US-09-621-976-15180
: Sequence 15180, Application US/09621976
: Patent No. 6539063
: GENERAL INFORMATION:
:   APPLICANT: Dumas Milne Edwards, J.B.
:   APPLICANT: Jobert, S.
:   APPLICANT: Giordano, J.Y.
:   TITLE OF INVENTION: ESTs and Encoded Human Proteins.
:   FILE REFERENCE: GENSET_054FR2
:   CURRENT APPLICATION NUMBER: US/09/621,976
:   CURRENT FILING DATE: 2000-07-21
:   NUMBER OF SEQ ID NOS: 19335
:   SOFTWARE: Patent .pm
:   SEQ ID NO 15180
:   LENGTH: 463
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURE: misc_feature
:   LOCATION: 74
:   OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15180

Alignment Scores:
Pred. No.: 2e-51 Length: 463
Score: 55.00 Matches: 55
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 50.9% Indexes: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-621-976-15180 (1-463)

: SEQ ID NO 54
: LENGTH: 73
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: misc_feature
: NAME/KEY: misc_feature
: LOCATION: 20
: OTHER INFORMATION: k=g or t
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 38
: OTHER INFORMATION: s=g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 79
: OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-10371

Qy 54 IleGluCysGlnAlaSerGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
Db 103 ATAGAATGTCAGCTAACCGTGGTACTCTGAAAGGTGACTGTGCATGGGA 162

Qy 74 ValCysSerHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
Db 163 GTCTGPAACCATGCTTCACTGCCACTGTCTGCTGGCTAAACACGACAGGTG 222

Qy 94 CysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGlyHis 108
Db 223 TGTCATTGGACAACAGAGTGGAATTCCAAAAGATGGCAC 267

RESULT 11
US-09-313-294A-492
: Sequence 492, Application US/09313294A
: Patent No. 6476212
: GENERAL INFORMATION:
:   APPLICANT: Laligudi, Raghunath V.
:   APPLICANT: Ito, Laura Y.
:   APPLICANT: Sherman, Bradley K.
:   TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
:   CURRENT APPLICATION NUMBER: US/09/313,294A
:   CURRENT FILING DATE: 1999-05-14
:   NUMBER OF SEQ ID NOS: 7600
:   SOFTWARE: PERL program
SEQ ID NO 492
Length: 301
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 7005493335H1
US-09-313-294A-492

Alignment Scores:
Pred. No.: 3.95e-35 Length: 301
Score: 40.00 Matches: 40
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 37.0% Indexes: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-313-294A-492 (1-301)
Qy 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaAspAlaCysAlaIle 44
Db 181 AAGAAGTGGAAACGCCGTCGGCATGGATATCTCGCTGACACTGGCTATC 240

Qy 45 CysArgAsnHisIsoleMetAspLeuCysIleGlucySGlnAlaAlaGlnAlaSerAlaThr 64
Db 241 TGCCGCAACACATCATGGATCTATGATCATGCTGAGGCCAGGGAAACAAACGCGGAC 300

RESULT 12
US-09-949-016-16682
: Sequence 16682, Application US/09949016
: Patent No. 6812319
: GENERAL INFORMATION:
:   APPLICANT: Venter, J. Craig et al.
:   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
:   CURRENT APPLICATION NUMBER: US/09/949,016
:   CURRENT FILING DATE: 2000-04-14
:   PRIORITY NUMBER: 60/241,755
:   PRIOR FILING DATE: 2000-10-20
:   PRIORITY NUMBER: 60/237,768
:   PRIOR FILING DATE: 2000-10-03
:   PRIORITY NUMBER: 60/231,498
:   PRIOR FILING DATE: 2000-09-08
:   NUMBER OF SEQ ID NOS: 207012
:   SOFTWARE: Fastseq For Windows Version 4.0

```

```

; SEQ ID NO 16682
; LENGTH: 25274
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16682

Alignment Scores:
Pred. No : 2.668e-21 Length: 25274
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.9% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-016-16682 (1-25274)
QY    77 HisAlaPheHisCysIleSerArgGlnValCysProLeu 96
Db     18411 CATGCTTTCACTTCACATCCATCTCGTGGCTCAAAACGACAGGTGTCCATTG 18470

QY    97 AspAsnArgGluTrpGluPheGlnIys 105
Db     18471 GACAACAGAGTGGAATTCCAAAAG 18497

RESULT 13
US-09-914-324A-4
; Sequence 4, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Kamura, Ronald C.
; APPLICANT: Kamura, Takumi
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(369)
; OTHER INFORMATION: Rbx1
US-09-914-324A-4

Alignment Scores:
Pred. No.: 0.00033 Length: 480
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-324A-4 (1-480)
QY    39 ValAspAsnCysAlaIleCysArgAsnHistileMet 50
Db     157 GTTGACAACTGTGCATTGCAAGAACATAATG 192

RESULT 14
US-09-270-767-26812/c
; Sequence 26812, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26812
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26812

Alignment Scores:
Pred. No.: 0.000337 Length: 490
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-270-767-26812 (1-490)
QY    39 ValAspAsnCysAlaIleCysArgAsnHistileMet 50
Db     256 GTGACAACTGTGCCATCTGCCGTAACCACATCTG 221

RESULT 15
US-09-270-767-111265/c
; Sequence 11265, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11265
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-111265

Alignment Scores:
Pred. No.: 0.000704 Length: 1101
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-270-767-111265 (1-1101)
QY    39 ValAspAsnCysAlaIleCysArgAsnHistileMet 50
Db     867 GTGACAACTGTGCCATCTGCCGTAACCACATCTG 832

Search completed: March 11, 2006, 09:40:59
Job time : 171 secs

```

Copyright GenCore version 5.1.7  
(c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 11, 2006, 09:45:04 ; Search time 653 Seconds  
(without alignments)

Scoring table: OLIIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 12

Total number of hits satisfying chosen parameters: 119

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

```
-MODEL=frame_p2n.model -DEV=x1h
-O=/abs/ABSSW_spool/US09541462/runat_10032006_080844_22623/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=o190.rnpbm
-MINMATCH=0.1 -LOOPC1=0 -LOOPC2=0 -UNITS=bits -START=-1 -END=-1 -MATRIX=oligo
-TRANS=human40_cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality
-ALIGN=15 -MODE=LOCAL -OUTFMT=ext -NORM=ext -HEAPSZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs100h
-NO_MMAP -NBG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=60 -XGAPEXT=60 -FGAPPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
```

Database : Published\_Applications\_NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB..seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB..seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB..seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB..seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB..seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB..seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB..seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match	Length	DB ID	Description
1	108	100.0	433	7	US-10-242-535A-43377	Sequence 43377, A
2	108	100.0	433	7	US-10-242-535A-43377	Sequence 43377, A
3	108	100.0	453	7	US-10-242-535A-5025	Sequence 35025, A
4	108	100.0	453	7	US-10-085-783A-55025	Sequence 35025, A
5	108	100.0	467	7	US-10-242-535A-39933	Sequence 39933, A
6	108	100.0	467	7	US-10-085-783A-39933	Sequence 39933, A
7	108	100.0	471	7	US-10-242-535A-57254	Sequence 57254, A

**ALIGNMENTS**

RESULT 1  
; Sequence 43377, Application US/10242535A  
; Publication No. US2004013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; C. C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10-242, 535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIORITY APPLICATION NUMBER: US 10/085, 783  
; PRIORITY FILING DATE: 2002-02-28  
; PRIORITY APPLICATION NUMBER: US 60/305, 340  
; PRIORITY FILING DATE: 2001-07-13  
; PRIORITY APPLICATION NUMBER: US 60/275, 017  
; PRIORITY FILING DATE: 2001-03-12  
; PRIORITY APPLICATION NUMBER: US 60/271, 955  
; PRIORITY FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58934  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 43377  
; LENGTH: 433  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-242-535A-43377  
Alignment Scores: 9,41e-111  
Pred. No.: 108 00  
Score: 108 00  
Percent Similarity: 100.0%

Best Local Similarity: 100.0%  
 Query Match: 100.0%  
 DB: 7

US-09-541-462B-2 (1-108) × US-10-242-535A-43377 (1-433)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 20 ATGGCGCACCGATGTGATAACGGATACCCAGGGAAAGAG 79

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeutPralaTrpAspIleValAsp 40  
 Db 80 CGCTTGTAGTGAAGTAAAAGTGAAATGCAAGTGGCTGGATATTGCGTTGAT 139

Qy 41 AsnCysAlaLysCysArgAnHiSileAspLeuCysIleGluCysGlnAlaAsnGln 60  
 Db 140 AACITGCCCATCTGAGAACCCATTTGATAGATGTAAGCTAACCG 199

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHiSalaPheHis 80  
 Db 200 GCGTCGGCTACTCTGAAAGTGTGACTCTGGAACTCTGTAACCCTTCAC 259

Qy 81 PheHiCysS1leSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 260 TTCCACTGCATCTCTGCTGTCATGGTGTGTCATTGGACAAACAGAG 319

Qy 101 TrpGluPheGlnLysTygLyHis 108  
 Db 320 TGGGAATTCCAAAAGTAGTGGCAC 343

RESULT 3

US-10-242-535A-35025  
 ; Sequence 35025, Application US/10242535A  
 ; Publication No. US2004013663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; Liew, C. C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2005  
 ; CURRENT APPLICATION NUMBER: US/10/242,535A  
 ; CURRENT FILING DATE: 2002-09-12  
 ; PRIORITY NUMBER: US 10/085,783  
 ; PRIORITY FILING DATE: 2002-02-28  
 ; PRIORITY NUMBER: US 60/305,340  
 ; PRIORITY NUMBER: 4231/2005  
 ; PRIORITY NUMBER: US 60/275,017  
 ; PRIORITY NUMBER: 2001-03-12  
 ; PRIORITY NUMBER: US 60/271,955  
 ; PRIORITY NUMBER: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 35025  
 ; LENGTH: 453  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-242-535A-35025

Alignment Scores:  
 Pred. No.: 9.79e-111 Length: 453  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservativeness: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-242-535A-35025 (1-433)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysLys 20  
 Db 24 ATGGCGCACCGATGTGATAACGGCTGGATACCCAGGCCACCRACAGGGCGCGCAAGAAG 83

Alignment Scores:  
 Pred. No.: 9.41e-111 Length: 433  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-085-783A-43377 (1-433)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyAlaGlyLysLys 20  
 Db 20 ATGGCGCACGCCATGGTGTGGATACCCAGGGCAACAGGGCGGGCAAGAG 79

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeutPralaTrpAspIleValAsp 40  
 Db 80 CGCTTGTAGTGAAGTAAAAGTGAAATGCAAGTGGCTGGCTGGATATTGCGTTGAT 139

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaLeutPralaTrpGlyValCysAsnHiSalaPheHis 80  
 Db 204 GCGTCGGCTACTCCAGTACTGAACTGGGAGTCATGGCTGCTGAACTCATGCTTTCAC 263

Qy 81 PheHiCysS1leSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 264 TTCCACTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGATGCTGGCTGGATATTGCGTTGAT 323





Db 197 GCGTCCGTACTTCAGAAGTGACTGCAATGGGAGTCGTGAACTGCTTTAC 256  
 Qy 81 PheHisCysIleSerArgTrpLeuThrArgGlnValCysProLeuAsnArgGlu 100  
 Db 257 TCCACTGCATCTGGCTCAAACAGCTGGTCATGGACACAGAG 316  
 Qy 101 TrpGlutPheGlnLysTrpGlyHis 108  
 Db 317 TCGGAATTCCAAAAGTAGTGGCAC 340

---

**RESULT 9**  
 US-10-242-535A-56068  
 ; Sequence 56068, Application US/10242535A  
 ; Publication No. US20040013661A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; ATTORNEY: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085, 783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIORITY NUMBER: US 60/305, 340  
 ; PRIORITY FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275, 017  
 ; CURRENT FILING DATE: 2002-09-12  
 ; PRIOR APPLICATION NUMBER: US 10/085, 783  
 ; PRIOR FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/305, 340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275, 017  
 ; LENGTH: 472  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (437)-(437)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; SEQ ID NO: 56068

**RESULT 10**  
 US-10-085-783A-56068  
 ; Sequence 56068, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; ATTORNEY: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085, 783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIORITY NUMBER: US 60/305, 340  
 ; PRIORITY FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275, 017  
 ; CURRENT FILING DATE: 2002-09-12  
 ; PRIOR APPLICATION NUMBER: US 10/085, 783  
 ; PRIOR FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/271, 955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 56068

Alignment Scores:  
 Pred. No.: 1.02e-110 Length: 472  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-085-783A-56068 (1-472)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
 Db 20 ATGGCCGAGCATGGTGGATACTCCGAGGCCACAGGGCGGGAGAG 79

Alignment Scores:  
 Pred. No.: 1.02e-110 Length: 472  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-242-535A-56068 (1-472)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
 Db 21 ArgPheGluValLysTrpAsnAlaLeuTrpAlaTrpAspIleValAsp 40  
 DB: 80 CGCTTCTTAAAGTCAAAGTGAATGGCTGGGATATTGGTGGTAT 139

Qy 21 ArgPheGluValLysTrpAsnAlaLeuTrpAlaTrpAspIleValAsp 40  
 Db 20 ATGGCCGAGCATGGTGGATACTCCGAGGCCACAGGGCGGGAGAG 79

Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeucysIleGluCysGlnAlaAsnGln 60  
 Db 200 GCGTCGGCTACTTCGAAAGTGTACTGTCGATGGGAGTCGTGTAACATGTTTCAC 259

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAsnArgGlu 100  
 Db 140 AACCTGCCCCATCTGCAGGAACCACATTATGCAATGTCAGCTAACCCAG 199

Qy 61 AlaSerAlaIleSerGluGlucysTrpValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 260 TCCACTGCATCTGCCTGCTGCTGCTAACACGCAACGCTGTCATTTGCAATGTCAGCTAACCCAG 319

Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 320 TGGGAAATTCCAAAAGTAGTGGCAC 343

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAsnArgGlu 100

RESULT 11  
US-10-913-937-5  
Sequence 5, Application US/10913937  
Publication No. US20050019813A1  
GENERAL INFORMATION:  
APPLICANT: Conway, Joan A.  
APPLICANT: Conway, Ronald C.  
APPLICANT: Kamura, Takumi  
APPLICANT: Oklamona Medical Research Foundation  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/10/913,937  
CURRENT FILING DATE: 2004-08-05  
PRIOR APPLICATION NUMBER: US/09/914,324  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: US 60/121,787  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/10/913,937  
CURRENT FILING DATE: 2004-08-15  
PRIOR APPLICATION NUMBER: US/09/914,324  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: US 60/121,787  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: WO PCT/US00/04838  
NUMBER OF SEQ ID NOS: 12  
PRIOR FILING DATE: 2000-02-25  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 504  
TYPE: DNA  
ORGANISM: Mus sp.  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (18)..(344)  
OTHER INFORMATION: Rbx1  
US-10-913-937-5

Alignment Scores:  
Pred. No.: 1.08e-110 Length: 504  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 8 Gaps: 0  
DB: US-10-913-937-5

US-09-541-462B-2 (1-108) × US-10-913-937-3 (1-508)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
DB 18 ATGGCCGGGGATGTGATTCGCCAGCAGGGCAACGGGGAGAGAG 77

QY 21 ArgPheGluValLysLysTPAsnAlaValAlaLeutTPAlaTPAspIleValValAsp 40  
DB 78 CGCTTGAAAGTTAAAAGTGAATGCGAATGCGCTGGCACATTGTGCTTGAT 137

QY 41 AsnCysAlaAlaCysArgAsnHist1MetAspLeuCysIleGluCysGlnAlaAsnGln 60  
DB 138 AACGTGCCATCTGCAGAACCATTAIGATCTTGTATGCAATGGCCAACACAG 197

QY 61 AlaSerAlaThrSerGluCysIleGluCysSerGlyValCysAsnHisAlaPheHis 80  
DB 198 GCGTCAGCTACTCCAAAGACTGTACGGTTCATGGCAATGCTGCTCAAACAGAGAG 317

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
DB 258 TTCCACTGCACTCTCGATGCTGGCAACGGCAGGGTCTGGTGGCAACAGAGAG 341

RESULT 12  
US-10-913-937-3  
Sequence 3, Application US/10913937  
Publication No. US20050019813A1  
GENERAL INFORMATION:  
APPLICANT: Conway, Joan A.

APPLICANT: Conaway, Ronald C.  
APPLICANT: Kamura, Takumi  
APPLICANT: Oklamona Medical Research Foundation  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/10/913,937  
CURRENT FILING DATE: 2004-08-05  
PRIOR APPLICATION NUMBER: US/09/914,324  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: US 60/121,787  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: WO PCT/US00/04838  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 508  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (7)..(333)  
OTHER INFORMATION: Rbx1  
US-10-913-937-3

Alignment Scores:  
Pred. No.: 1.08e-110 Length: 508  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 8 Gaps: 0  
DB: US-10-913-937-3

US-09-541-462B-2 (1-108) × US-10-913-937-3 (1-508)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
DB 7 ATGGCCGGGGCGAGGGATGTGGATACCCGAGCCACAAACAGGGCCAGGAGAG 66

QY 21 ArgPheGluValLysLysTPAsnAlaValAlaLeutTPAlaTPAspIleValValAsp 40  
DB 67 CGCTTGAACTGTAAGAAAGTGAATGCGATCTGGCTGGGATATTGCTGTGAT 126

QY 41 AsnCysAlaAlaCysArgAsnHist1MetAspIleCysIleGluCysGlnAlaAsnGln 60  
DB 127 AACGTGCCATCTGCAGAACCATTAIGATCTTGTATGAGATGCACTGGTACACAG 186

QY 61 AlaSerAlaThrSerGluCysIleGluCysSerGlyValCysAsnHisAlaPheHis 80  
DB 187 GCGTCAGCTACTCCAAAGACTGTACGGTTCATGGCAATGCTGCTCAAACAGAGAG 246

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
DB 247 TTCACTGCACTCTGCCTGGCTCAAACAGAGAG 306

RESULT 13  
US-10-242-535A-46292  
Sequence 46292, Application US/10242535A  
Publication No. US200401363A1  
GENERAL INFORMATION:  
APPLICANT: ChondroGene Inc.  
APPLICANT: Lieuw, C.C.  
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
FILE REFERENCE: 4231/2005  
CURRENT APPLICATION NUMBER: US/10/242,535A  
CURRENT FILING DATE: 2002-09-12  
PRIOR APPLICATION NUMBER: US 10/085,783  
PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340  
 i PRIOR FILING DATE: 2001-07-13  
 i PRIOR APPLICATION NUMBER: US 60/275,017  
 i PRIOR FILING DATE: 2001-03-12  
 i PRIOR APPLICATION NUMBER: US 60/271,955  
 i PRIOR FILING DATE: 2001-02-28  
 i NUMBER OF SEQ ID NOS: 58994  
 i SOFTWARE: PatentIn version 3.2  
 i SEQ ID NO: 46292  
 i LENGTH: 523  
 i TYPE: DNA  
 i ORGANISM: Human  
 US-10-242-535A-46292

Alignment Scores:  
 Pred. No.: 1.11e-110 Length: 523  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-46292 (1-523)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLys 20  
 Db 19 ATGGCCAGCAGCATGGTGTGATACCCGAGCGAACACAGCGGGACCACAGCGGGCAAGAAG 78

Alignment Scores:  
 Pred. No.: 1.11e-110 Length: 523  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-46292 (1-523)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLys 20  
 Db 19 ATGGCCAGCAGCATGGTGTGATACCCGAGCGAACACAGCGGGACCACAGCGGGCAAGAAG 78

Qy 21 ArgPheGluValLysTrpAsnAlaValTrpAspIleValAsp 40  
 Db 79 CGCTTAAAGTGAAGTAAAGTGTGATGGCTGAGTCAGTGCCTGGATATGTGGTTGAT 138

Qy 41 AsnCysAlaLeuCysArgAsnHisIleMetAspLeuCysIle 60  
 Db 139 AACTGCCATCTGAGAACACATTATGATCTTGATAGTCAGCTAACAG 342

RESULT 15  
 US-09-918-995-17191  
 i Sequence 17191, Application US/09918995  
 i Publication No. US20030073623A1  
 i GENERAL INFORMATION:  
 i APPLICANT: Hyseq, Inc.  
 i TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 i FROM VARIOUS cDNA LIBRARIES  
 i FILE REFERENCE: 20411-756  
 i CURRENT APPLICATION NUMBER: US/09/918,995  
 i CURRENT FILING DATE: 2001-07-30  
 i PRIORITY APPLICATION NUMBER: US/09/235,076  
 i NUMBER OF SEQ ID NOS: 38054  
 i SOFTWARE: FastSEQ for Windows Version 3.0  
 i SEQ ID NO: 17191  
 i LENGTH: 476  
 i TYPE: DNA  
 i ORGANISM: Homo sapiens  
 i FEATURE:  
 i NAME/KEY: misc\_feature  
 i LOCATION: (1)..(476)  
 i OTHER INFORMATION: n = A,T,C or G

Qy 61 AlaSerAlaThrSerGluGlucySThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 199 GCTGCCCTACTCGATCCATGCTGTAAACCTGCTTAACATGCTTAC 258

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 259 TTCCACTGCATCTCGCTCAAAACGACAGGTGTTGTCATGGACAACAGAGAG 318

Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 319 TGGGATTCAAAAGTAGTGGCAC 342

RESULT 14  
 US-10-085-783A-46292  
 i Sequence 46292, Application US/10085783A  
 i GENERAL INFORMATION:  
 i APPLICANT: ChondroGene Inc.  
 i APPLICANT: Liew, C.C.  
 i TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 i FILE REFERENCE: 4231/2002  
 i CURRENT APPLICATION NUMBER: US/10/085,783A  
 i CURRENT FILING DATE: 2002-02-28  
 i PRIOR APPLICATION NUMBER: US 60/305,340  
 i PRIOR FILING DATE: 2001-07-13  
 i PRIOR APPLICATION NUMBER: US 60/275,017  
 i PRIOR FILING DATE: 2001-03-12  
 i PRIOR APPLICATION NUMBER: US 60/271,955  
 i PRIOR FILING DATE: 2001-02-28  
 i NUMBER OF SEQ ID NOS: 58994  
 i SOFTWARE: PatentIn version 3.2  
 i SEQ ID NO: 46292  
 i LENGTH: 523  
 i TYPE: DNA  
 i ORGANISM: Human  
 US-10-085-783A-46292

Qy	22	PheGluValLysTrpAsnAlaValAlaLeuTrpAlaIleTrpAspIleValAspAsn	41
Db	135	TTTGAAGTGAAAAGTGGATGAGTAGCCTCGGCTGGATATGTGGTGANAC	194
Qy	42	CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla	61
Db	195	TGTGCCATTGCAAGAACACATTGATCTTGCAAGATCTAACCTAACAGCG	254
Qy	62	SerAlaThrIleGluCysSerIleValAlaIleTrpGlyValCysAsnHisIleAlaPheHisIle	81
Db	255	TCCGCTACTTCAGAAGAGCTACTGCGATGGGAGCTGTAAACCAGCTTTCACTRC	314
Qy	82	HisCysIleSerArgTripleUlysThrArgGlnValCysProIleAspAsnArgGluIrp	101
Db	315	CACTGCATTCCTCGTGGCTAAACACGAGCTGTCATGGACACAGAGCTGG	374
Qy	102	GluPheGlnLysTrpGlyHis	108
Db	375	GAATTCAAAAGTGGCAC	395

Search completed: March 11, 2006, 10:04:09  
 Job time : 655 secs

Copyright GenCore version 5.1.7  
(c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 11, 2006 08:30:45 ; Search time 494 Seconds  
(without alignments)

Title: US-09-541-462B-2  
Perfect score: 108  
Sequence: 1 MAAMADVDTPSGTNSGAGKK.....KTRQVCPFLDNREWEFQKYGH 108

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996397 seqs, 3332346308 residues

Word size: 12

Total number of hits satisfying chosen parameters: 95

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

```
-M0DPL=frame_plus_p2n.model -DEV=1h
-Q=/abs/ABSSNBB/spool/US09511462/runat_10032006_080830_22345/app_query.fasta_1
-DB=N_Geneseq -QFORMAT=fasta -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40 cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=12 -ALIGN=15 -MODDB=LOCAL
-OUTFORMAT=proto -NORMI=ext -HEAPSIZEB=500 -MINLEN=0 -MAXLEN=100000000 -HOST=abs03h
-USER=@US09511462 @CCN 1.1 727 @runat 10032006 080830_22345 -NCPU=6 -TCPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=10 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=10 -THREADS=1 -XGAPOP=60 -XGAPEXT=7 -FGAPEXT=60 -FGAPOP=6
-YGAPOP=60 -YGAPEXT=60 -DELEXT=7
```

Database : N\_Geneseq.21:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2011as:\*
- 5: geneseqn2011bs:\*
- 6: geneseqn2012as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1.	108	100.0	327	3	AAA96882	Aaa96882 Nucleotid
2	108	100.0	482	3	AA03896	Aac03896 Human sec
3	108	100.0	504	3	AA74380	Aaa74380 DNA encod
4	108	100.0	506	12	ADQ87496	Adq87496 Human tum

## ALIGNMENTS

RESULT 1	ID	AAA96882	standard; DNA; 327 BP.
XX	AC	AAA96882;	
XX	XX		19-FEB-2001 (first entry)
XX	DE		Nucleotide sequence of human ring finger protein ROC1.
XX	KW		ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway;
KW	KW		cullin dependent ubiquitin ligase; CDK inhibitor Sici degradation; tumour; ss.
XX	OS		Homo sapiens
XX	PN		WO200058472-A2.
XX	FH		Key
XX	FT		CDS
FT	FT		/tag= "ROC1"
FT	PR		/product= "ROC1"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1.	108	100.0	327	3	AAA96882	Aaa96882 Nucleotid
2	108	100.0	482	3	AA03896	Aac03896 Human sec
3	108	100.0	504	3	AA74380	Aaa74380 DNA encod
4	108	100.0	506	12	ADQ87496	Adq87496 Human tum







6 ATGGCGCAGCCATGGATGGTGTGATACTCCGACGGCAACAGCGCGGGCAAGAAG 65  
 21 ArgPheGluValLysTrpAlaValAlaLeuTrpAlaTrpAspIleLeuValAsp 40  
 66 CGTTTGAGTGAANAGTGGATGCGTAGCCCTGGCTGGATATGGTTGAT 125  
 41 AsnCysAlaIleCysArgAspHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
 126 AACTTGTCATCGAGAACCATPATGGATCTTGATGCTAACGCTTACAG 185  
 61 AlaSerIleThrSerGluGlucLysThrValAlaIlePheGlyValCysBsnHisAlaPheHis 80  
 186 GCTCCGCTACTTCAGAGAGTGACTGTCATGGAGTCATGCTAACATGCTTAC 245  
 81 PheHistysIleSerGluGlucLysThrValAlaIlePheGlyAsnAsnArgGlu 100  
 246 TTCCACTGCATCTCCCTGGTCAAACAGACAGGGTGTGTCATTGGACAACAGAG 305  
 101 TrpGluIpheGlnLysTrpGlyHis 108  
 306 TGGAAATTCCAAAAGTATGGCAC 329

**RESULT 6**  
 ADQ84881 standard; cDNA; 506 BP.  
 XX

AC ADQ84881  
 XX  
 DT 07-OCT-2004 (first entry)  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1695.  
 XX  
 KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
 KW cancer; cell proliferative disorder; gene; ss.; gene therapy;  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004060270-A2.  
 XX  
 PD 22-JUL-2004.  
 XX  
 PF 15-OCT-2003; 2003WO-US029126.  
 XX  
 PR 18-OCT-2002; 2002US-041898P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD ) WU T D.  
 PA (ZHOU /) ZHOU Y.  
 XX  
 PI Wu TD; Zhou Y;  
 XX  
 DR WPI; 2004-534300/51.  
 XX  
 PT New nucleic acid molecule and encoded polypeptide, for diagnosing,  
 PT preventing or treating cell proliferative disorders such as cancer.  
 XX

Claim 1: SEQ ID NO 1695: 5504pp; English.

XX  
 CC The present invention describes an isolated tumour-associated antigenic  
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full length coding region of  
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
 CC sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) -  
 CC (c). Also described: (1) an expression vector comprising the above  
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
 CC a process for producing a polypeptide; (4) an isolated polypeptide  
 CC comprising: (a) an amino acid sequence encoded by any of the above  
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
 CC length coding region of the above nucleotide sequences; or (c) a sequence  
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
 CC an isolated antibody that binds to the above polypeptide; (7) a process

CC for producing the antibody; (8) an isolated oligopeptide that binds to  
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
 CC binding organic molecule that binds to the above polypeptide; (10) a  
 CC composition of matter comprising the above (chimeric) polypeptide,  
 CC antibody, oligopeptide or TAT binding organic molecule, in combination  
 CC with a carrier; (11) an article of manufacture comprising a container and  
 CC the composition of matter contained within the container; (12) methods of  
 CC inhibiting the growth of a cell that expresses the above protein, where  
 CC the growth of the cell is at least in part dependent upon a growth  
 CC potentiating effect of the above protein; (13) a method of  
 CC therapeutically treating a mammal having a cancerous tumour comprising  
 CC cells that express the above protein; (14) a method of determining the  
 CC presence of a protein in a sample suspected of containing the protein  
 CC described above; (15) methods of diagnosing the presence of a tumour in a  
 CC mammal; (16) a method for treating or preventing a cell proliferative  
 CC disorder associated with increased expression or activity of the above  
 CC protein; and (17) a method of binding an antibody, oligopeptide or  
 CC organic molecule to a cell that expresses the protein described above.  
 CC The TAT sequences have cytostatic activities, and can be used in gene  
 CC therapy. The composition and methods are useful for diagnosing,  
 CC preventing or treating cancer. The composition is also used for preparing  
 CC a medicament for the therapeutic treatment or diagnostic detection of a  
 CC cell proliferative disorder or cancer. The present sequence represents a  
 CC human TAT cDNA sequence from the present invention.  
 XX Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

SQ ADQ84881 standard; cDNA; 506 BP.  
 XX

Alignment Scores:  
 Pred. No.: 2.73e-106 Length: 506  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-541-462B-2 (1-108) x ADQ84881 (1-506)

Qy 1 MetAlaAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
 Db 6 ATGGCGCAGGGATGGATGGATGGATACCCCGAGGGCACCAAGCGGCCAGAAAG 65  
 Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaAspIleValAsp 40  
 Db 66 CGCTTGTAAAGTGAAGAAAAGTGAATGCTGGATATGGCTGGATATGGTTGAT 125  
 Qy 41 AsnCysAlaLysLysCysArgAlaHisIleMetAspIeuCysteIeuCysGlnAlaLysGln 60  
 Db 126 AACTRGCCCCATCTGGAAACCACATTAGGATAGTGTAGCTTGTACGCTTACCGAG 185  
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 186 GCGTCGGCTACTTCAGAAGAGTGTACTGTGCACTGGGACTCTGTAACTGCTTCAC 245  
 Qy 81 PheHisCysIleSerArgTrpLeuLysIleArgGlnValCysProLeuIleAsnArgGlu 100  
 Db 246 TTCCACTGCAATCTCGCTGGCTAAACACGCAAGGGTGTGTCATGGACAAAGAGAG 305  
 Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 306 TGGAAATTCCAAAAGTATGGCAC 329

RESULT 7  
 AAA74978 standard; DNA; 508 BP.  
 XX  
 AC AAA74978;  
 XX  
 DT 02-JAN-2001 (first entry)  
 DE DNA encoding a human cullin-interacting RING-H2 finger protein (Rbx1).  
 XX  
 KW Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;  
 KW tumour suppressor; carcinoma; Ring box associated carcinoma;

KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;  
KW cerebellar hemangioblastoma; hemangioma; retinal angioma;  
KW pheochromocytomas; ss.  
XX Homo sapiens.  
XX Location/Qualifiers  
Key CDS 7 .333  
FT /\*tag= a  
FT /product= "cullin-interacting RING-H2 finger protein  
FT (Rbx1)"  
XX WO2000050445-A1.  
XX PD 31-AUG-2000.  
XX PP 25-FEB-2000; 2000WO-US004838.  
XX PR 26-FEB-1999; 9US-0121787P.  
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
XX Conaway JA, Conaway RC, Kamura T;  
PI XX DR WPI: 2000-572067/53.  
DR P-PSDBB; AAB08813.  
XX Cullin interacting RING-H2 finger protein, a component of von Hippel-  
Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF)-  
ubiquitin ligase, useful for diagnosing and treating Ring box protein  
associated carcinomas.  
XX PS Claim 3; Page 35; 37pp; English.  
XX CC The present sequence encodes a human cullin-interacting RING-H2 finger  
CC protein (Ring box protein), designated Rbx1. The polypeptide is a tumour  
CC suppressor. Rbx1 is useful for diagnosing a predisposition of a patient  
CC to certain carcinomas. It is also useful for treating Ring box protein  
CC associated carcinomas or augmenting metabolically deficient system in  
CC animals. Rbx1 is also useful for evaluating the effectiveness of a  
CC therapeutic treatment for Ring box associated carcinomas. Rbx1 can be  
CC used to screen for agents which augment or inhibit the activity of other  
CC cullin-containing ubiquitin ligase and of the VHL (von Hippel- Lindau)  
CC complex controlling the conjugation of ubiquitin or ubiquitin-like  
CC proteins to various sets of target proteins. Carcinomas which may be  
CC treated include renal carcinomas, cerebellar hemangioblastomas and  
CC hemangiomas, retinal angioma and pheochromocytomas  
XX SQ Sequence 508 BP, 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerIylAlaGlyLysLys 20  
Score: 7 ATGGCGCAGCATGGATGGTGTGATAACCCGAGCGGACCACAGCGCCGGCAAGAG 66  
Percent Similarity: 100.0% Best Local Similarity: 100.0% Query Match: 100.0% DB:  
Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0

us-09-541-462B-2 (1-108) x AAA74978 (1-508)

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerIylAlaGlyLysLys 20  
7 ATGGCGCAGCATGGATGGTGTGATAACCCGAGCGGACCACAGCGCCGGCAAGAG 66  
21 ArgPheGluValLysIylTrpAsnAlaValAlaLeuIrpAlaTrpAspIleValAsp 40  
67 CACTCTGAACTGAAAATGCTGAAATGGATGGATGGCTGGCTGGATATGGTTGAT 126  
41 AsnCysAlaIleCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsnGln 60  
127 AACTGTCGCCATCTGCAGAACACATPATGATCATTCAGTCAAGCTAACAG 186  
61 AlaSerAlaIhrSerGluGluCysThrValAlaIrpIleValCysThrValAlaPheHis 80

Db 187 GC[GCGCTACTTCAGAGAGTACTCTGCATGGGAGAGTCGTAACTATGCTTTTCRC 246  
Qy 81 PheIscCysIleSerArgTrpLeuLysThrArgTrpGlnValCysProLeuAspAlaArgGlu 100  
Db 247 TTCACTGCATCTCTGCTGGCTCAAACACGAGCTGTCATTGGACAAACAGAGAG 306  
Qy 101 TrpGluIleGlnIlysTyrglyHis 108  
Db 307 TGGGAATTCCAAGATGGCAC 330

RESULT 8  
ACN40951 ID ACN40951 standard; cDNA; 508 BP.  
XX ACN40951:  
XX AC  
XX DT 18-NOV-2004 (first entry)  
XX DE Tumour-associated antigenic target (TAT) cDNA DNA3326980, SEQ ID NO: 6072.  
XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
KW central nervous system cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; melanoma; leukemia; hybridisation probe;  
KW chromosome identification; chromosome mapping; gene mapping;  
KW gene therapy; cytostatic; gene; ss.  
XX OS Homo sapiens.  
XX PN WO2004030615-A2.  
XX PN WO2004030615-A2.  
XX PD 15-APR-2004.  
XX PP 29-SEP-2003; 2003WO-US028547.  
XX PR 02-OCT-2002; 2002US-0414971P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Wu TD, Zhang Z, Zhou Y;  
XX DR WPI: 2004-347921/32.  
XX DR P-PSDBB; ABM82365.  
XX PT New tumor-associated antigenic target polypeptides and nucleic acids,  
PT useful in preparing a medicament for treating or detecting a  
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
PT prostate cancer or tumor.  
XX DR  
XX PS Claim 1; SEQ ID NO 6072; 7273pp; English.  
XX CC The invention relates to human tumour-associated antigenic target (TAT)  
CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
CC overexpressed in cancer tissues compared to normal tissues, and may thus  
CC serve as effective targets for the diagnosis and treatment of cancer in  
CC mammals. The invention also relates to nucleic acid and polypeptide  
CC sequences at least 80% identical to the TAT nucleic acids and  
CC polypeptides, expression vectors and host cells comprising a TAT nucleic  
CC acid; an antibody specific for TAT polypeptide; fusion proteins comprising a  
CC molecule which binds to a TAT polypeptide; and methods and compositions for the treatment or  
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT nucleic acid of the invention.

XX Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;

SQ antisense DNA or RNA.

Alignment Scores:

Pred. No.: 2.74e-106	Length: 508
Score: 108.00	Matches: 108
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
DB: 13	Gaps: 0

US-09-541-462B-2 (1-108) x ACN0951 (1-508).

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
Db 7 ATGGCCGAGCCATGGATGGTGTGGATAACCCGAGCGGCCAACAGCGGCCAGAAG 66

Qy 21 ArgPheCleuLysLysIstPasnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
Db 67 CGCTTTCAGTGAAGAAAATGGAAATGCAATGCCCTCTGGCTGGATATGGTTGAT 126

Qy 41 AsnCysAlaIleCysArgAsnIleMetAspLeucystileGlucysGlnAlaAsnGln 60  
Db 127 AAC TGCCCATCTGCAGAACCATATTGATCTTGATAGAATGTCAGCTAACAG 186

Qy 61 AlaSerAlaThrSerGluGlySerAlaTropGlyValCysAsnHisAlaPheHis 80  
Db 187 GCGTCCCTACTCTCAGAGAGTGTACTGTCCATGGGAGSTCTGTGAACTGTTAC 246

Qy 81 PheHisCysIleSerArgPheLeuAspAsnLysProLeuAspAsnArgGlu 100  
Db 247 TTCCACTGCACITCTCGCTCAAACAGACAGGTGTCCATTGGCAACAGAGAG 306

Qy 101 TrpGluPheGinLysTrpGlyHis 108  
Db 307 TGGAAATTCCAAAAGTAGTGGCAC 330

RESULT 9

ID ACH29979 standard: cDNA; 476 BP.

XX Human; **SS**; sequencing by hybridisation; SBH; expressed sequence tag; EST;

AC ACH29979;

XX Genome mapping; biodiversity; genetic disorder.

DT 13-OCT-2003 (first entry)

XX Homo sapiens.

DE Human testis cDNA #365.

XX US2003073623-A1.

XX 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.

XX 30-JUL-2001; 2001US-00918995.

XX (DRM) DRMANAC R. T.

PA (LABA) LABAT I.

PA (STAC) STACHE-CRAIN B.

PA (DICK) DICKSON M. C.

PA (JONE) JONES L. W.

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

DR WPI: 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating

PT XX Claim 1; SEQ ID NO 17191; 44DP; English.

PS XX

XX The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH5031, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030073623

SQ Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;

XX

Alignment Scores:

Pred. No.: 3.05e-105	Length: 476
Score: 107.00	Matches: 107
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 99.1%	Indels: 0
DB: 9	Gaps: 0

US-09-541-462B-2 (1-108) x ACH29979 (1-476)

Qy 2 AlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 21  
Db 75 GCGGAGCGATGGATACCCTGAGGGCACCAACAGGGGGCAAGAGCGC 134

Qy 22 PheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAspAsn 41  
Db 135 TTGGAGTGAAACTGGATGCTACTGCTCTGGGATATTGGTGTATAAC 194

Qy 42 CysAlaIleCysArgAsnHistoleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61  
Db 195 TGTCGCACTGAGAAACCACATTATGGATCTTGTCATAGATGTCAGTAACCAGGGC 254

Qy 62 SerAlaThrSerGluGluCysThrValAlaItpGlyValCysAlaAlaPheHisPhe 81  
Db 255 TCCGGTACTCTCAGAAGAGTACTGTCATGGGAGTCATGTTCTGTAACCATGTTCTACATTC 314

Qy 82 HisCysIleSerArgTrpIleLeuIleGluCysGlnValCysProLeuAspAsnArgIleTrp 101  
Db 315 CACTCATCTCTCGTGGCTCAAACAGACAGGTGTCCATGGACAACAGAGGTGG 374

Qy 102 GluPheGlnLysTrpIleLeuIleGluCysGlnValCysProLeuAspAsnArgIleTrp 108  
Db 375 GAATCCAAAGATGGGCAC 395

RESULT 10

ADS0913\_C

ID ADS0913 standard; DNA; 3726 BP.

XX

AC ADS0913:

XX 16-DEC-2004 (first entry)

XX Human therapeutic DNA - SEQ ID 150.

KW antiinflammatory; neuroprotective; haemopoiesis; immunity; neurodegenerative; stem cell;

KW inflammatory; haematopoiesis; cancer; wound healing; gene therapy; db; gene.

XX Homo sapiens.

XX XX ACN90161;  
 XX XX ACN90161;  
 XX DT 02-DEC-2004 (first entry)  
 XX DE Breast cancer related marker, seq id 11311.  
 XX DE  
 XX KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.  
 XX OS Homo sapiens.  
 XX PN US2003099974-A1.  
 XX PD 29-MAY-2003.  
 XX PP 18-JUL-2002; 2002US-00198846.  
 XX PR 18-JUL-2001; 2001US-0306220P.  
 XX PA (MILL-) MILLENNIUM PHARM INC.  
 XX PI Lillie J, Xu Y, Wang Y, Steinmann K;  
 XX WPI; 2003-787014/74.  
 XX Disclosure; SEQ ID NO 11311; 36pp; English.  
 XX Novel isolated polypeptide associated with breast cancer, useful for breast  
 PT PT detecting presence of polypeptide in sample, as a marker for breast  
 PT cancer.  
 XX CC The invention relates to an isolated polypeptide (I) associated with  
 PT PT breast cancer which is encoded by a nucleic acid molecule comprising a  
 PT nucleotide sequence (S1). Further disclosed is an antibody that binds to  
 CC the polypeptide of the invention. The activity of the polypeptide of the  
 CC invention may be described as cytostatic. The antibody is useful for  
 CC detecting the presence of (I) in a sample. Nucleic acid molecules of the  
 CC invention are useful in the detection of breast tumors. (I) is useful as  
 CC a marker for breast cancer and in breast cancer therapy. Sequences given  
 CC in records ACN78851-ACN92934 represent nucleic acid markers associated  
 CC with breast cancer. Note: The sequence listing does not form part of the  
 CC specification but may be obtained in electronic format from the USPTO web  
 site at seqdata.uspto.gov/sequence.html?DocID=2003009974  
 XX SQ Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;  
 XX Alignment Scores:  
 Pred. No.: 2.43e-103 Length: 3726  
 Score: 106 Matches: 106  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 98.1% Indels: 0  
 DB: 13 Gaps: 0  
 XX SQ Sequence 4543 BP; 1069 A; 1171 C; 1083 G; 1220 T; 0 U; 0 Other;  
 XX Alignment Scores:  
 Pred. No.: 2.93e-103 Length: 4543  
 Score: 106.00 Matches: 106  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 98.1% Indels: 0  
 DB: 11 Gaps: 0  
 US-09-541-462B-2 (1-108) × ACN90161 (1-4543)  
 QY 3 AlaAlaMetAspValAspThrProSerGlyIleGlyLysLysArgPhe 22  
 DB 492 GCAGCGATGGATGGATACCCGAGGCCAAACAGCAGAACGGCTTT 433  
 QY 23 GluvalylsystTrpAsnAlaLeuTrpAlaTrpAspIleValAspAsnCys 42  
 DB 432 GAAGTGAAAAGTGGATGGCAGTAGCCCTGGGTGGATATGGTGTGATGT 373  
 QY 43 AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaser 62  
 DB 372 GGCATTCGCAAGAACCCATTGGAACTTGTAGAATGTCAGCTAACGCCGCC 313  
 QY 63 AlanThrSerGluGluCysIleValAlaTrpGlyValCysSerHisAlaPheHisPheHis 82  
 DB 312 GCTACTTCAGAAGCTACTGCGATGGCGAGTCTGTAACCCTTTCACCTCAC 253  
 QY 83 CysIleIleArgTrpLeuLysIleValArgInAlaCysProLeuAspSerArgGluGlu 102  
 DB 252 TGCATCTCTGCTGGCTAAACACGAGCTGGTGTGTCATGGACACAGAGTCGA 193  
 QY 103 PheGlnIleIleTrpGlyHis 108  
 DB 192 TTCCAAPAGTATGGCAGC 175  
 RESULT 11  
 ACN90161/c standard; DNA; 4543 BP.  
 ID ACN90161

Db 845 TGCAATCTCTGGCTAAACACGACAGGTTGTCTTGGAGAGTGAA 786  
 Qy 103 PheGlnIystCylHis 108  
 XX  
 Db 785 TTCCAAAAGTATGGCAC 768  
 RESULT 12  
 ADDQ92179  
 ID ADDQ92179 standard; DNA; 503 BP.  
 XX  
 AC ADQ92179;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Human autoantigen DNA fragment MPMGP800L05536.  
 XX  
 KW ds; autoantigen; antibody; hybridoma; biosensor chip;  
 KW extracorporeal differential diagnosis; autoimmune disease;  
 KW ribosomal protein; tubulin;  
 KW dolichyl-diphospho-oligosaccharide-glycosyl transferase;  
 KW multiple sclerosis; rheumatoid arthritis; epitope mapping;  
 KW affinity chromatography; electrophoresis; autogambody apheresis;  
 KW RNA interference; RNAi.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004058972-A1.  
 XX  
 PD 15-JUL-2004.  
 XX  
 PF 23-DEC-2002; 2002WO-EP014731.  
 XX  
 PR 23-DEC-2002; 2002WO-EP014731.  
 XX  
 PA (THIESEN H.  
 (LORENZ) LORENZ P.  
 XX  
 PI Thiessen H., Lorenz P;  
 XX  
 DR WPI; 2004-543459/52.  
 XX  
 FT New human DNA autoantigens, useful as assay, diagnostic, and prognostic  
 reagents and for treating autoimmune disease, also related expression  
 products and antibodies with similar uses.  
 XX  
 PS Claim 1; SEQ ID NO 160; 110pp; German.  
 XX  
 CC This invention describes novel human DNA autoantigens which are used to  
 CC produce recombinant expression vectors; prokaryotic or eukaryotic cells;  
 CC poly- or mono-clonal antibodies (Ab); specific; hybridomas that express  
 CC monoclonal Ab; biosensor chips having an addressable sequence pattern as  
 CC probe; medical or diagnostic instruments that include the biosensor; for  
 CC extracorporeal differential diagnosis of autoimmune diseases and  
 CC predisposition to them. The autoantigenic polynucleotides encode ribosomal  
 CC proteins; tubulins; dolichyl-diphospho-oligosaccharide glycosyl  
 CC transferases and proteins. The antibodies may be labelled conventionally  
 CC with radioisotopes, coloured or fluorescent groups, or a member of the  
 CC biotin/avidin pair, or colloidal gold. The autoantigens can be directed  
 CC against mitochondria, liver-kidney microsomes; histidine-tRNA; nuclear  
 CC membrane; neutrophilin/cytoplasm; insect cells; epidermal intracellular  
 CC or basal membrane antigens; Golgi or cell nuclei, or associated with  
 CC multiple sclerosis or rheumatoid arthritis. They are useful for epitope  
 CC mapping; in affinity chromatography or electrophoresis; for diagnosis,  
 CC prognosis, control of treatment or therapeutic response of autoimmune  
 CC diseases, particularly in vitro differential diagnosis of autoimmune  
 CC diseases; to produce biosensor chips or for therapeutic apheresis.  
 CC Autoantigenic DNA can be used for therapeutic RNA interference against  
 CC autoantibodies. Biochips that carry the new materials are useful in  
 CC medical and diagnostic instruments. ADQ92020-ADQ92280 represent human  
 CC autoantigens.  
 XX  
 SQ Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;

Alignment scores:  
 Pred. No.: 4.47e-103 Length: 503  
 Score: 105.00 Matches: 105  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 97.2% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-541-462B-2 (1-108) x ADQ92179 (1-303)  
 Qy 4 AlaMetAspPvalAspThrProserGlyThrAsnserGlyAlaGlyIysLYBargPheGlu 23  
 Db 3 GCGATGGATGTGGATAACCCGAGCGSACCAAAGGGCAGAAGCGCTTGAA 62  
 Qy 24 ValLysIystTPasnAlaValAlaLeuTrpAlaLysPaspIleValLysAsnCysAla 43  
 Db 63 GAGAAAGATGGATGAGTCAGTAGGCCCTGGCCCTGGGATATTGGCTTGTAACTGCC 122  
 Qy 44 IleCysArgAsnHsileMetAspLeuCysGlnAlaLysGlnAlaSerAla 63  
 Db 123 ATCTGGAGAACACATTTATGCTAGATGTCAGCTAACAGCGTCGGCT 182  
 Qy 64 ThrserGluCysIystValAlaTrpGlyValCysAsnHisAlaSerHisIysCys 83  
 Db 183 ACTTCGAAGAGTGTACTTGCCATGGGAGTCTGTTACCATGTTTCACTCCACTGC 242  
 Qy 84 IleSerArgTrpLeuIystArgGlnValCysProLeuAspAspArgGluTrpGluPhe 103  
 Db 243 ATCTTCGCTGGCTCAAAACGAGACGGTGTCCATTGGACAACAGAGACTGGGATTC 302  
 Qy 104 GlnLysIystGlyHis 108  
 Db 303 CAAAGTATGGCAC 317  
 RESULT 13  
 AAH97860 standard; DNA; 539 BP.  
 ID AAH97860  
 XX  
 AC AAH97860;  
 XX  
 DT 10-OCT-2001 (first entry)  
 DE Murine 7-transmembrane G-protein coupled receptor coding sequence #104.  
 XX  
 KW Murine; hematopoietic stem cell; signalling; vaccine; 7TM-GPCR;  
 KW 7-transmembrane G-protein coupled protein receptor; ds.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200160999-A1.  
 XX  
 DR 2001-09-26.  
 XX  
 FT Murine 7-transmembrane G-protein coupled receptor coding sequence #104.  
 XX  
 PR 14-FEB-2000; 2000US-0182377P.  
 XX  
 PA (IMCL-) IMCLONE SYSTEMS INC.  
 PA (UPR-) UNIV PRINCETON.  
 XX  
 PI Lemischka IR, Witte L, Pereira DS;  
 XX  
 DR WPI; 2001-522396/57.  
 XX  
 PT DNA sequences encoding 7-transmembrane G-protein coupled protein  
 PT receptors characteristic of hematopoietic stem cells, useful for treating  
 PT leukemia.  
 XX  
 PS Claim 1; Page 62; 176pp; English.  
 XX  
 CC The present invention relates to murine coding sequences for 7-  
 CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The  
 CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The



XX PR 17-FEB-2000; 2000US-0183319P.  
 PR 16-MAR-2000; 2000US-0189862P.  
 PR 25-MAY-2000; 2000US-0207454P.  
 PR 09-JUN-2000; 2000US-0211314P.  
 PR 18-JUL-2000; 2000US-0219007P.  
 PR 13-DEC-2000; 2000US-0255281P.  
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endge WO, Monahan JE;  
 XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 5119-5120; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV2213) of the specification or its complement. (1) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 4476 BP; 1085 A; 1129 C; 1015 G; 1247 T; 0 U; 0 Other;

Alignment Scores:

Bred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	4.75e-100	103.00	100.0%	95.4%	5	4476	103	0	0	0	0

US-09-541-462B-2 (1-108) x ABV25615 (1-4476)

Oy 3 AlaAlaLysAspValAlaProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22  
 Db 1014 GCAGCGTGGATGGATTACCCGGGGCACAAAGGGGGGCGCAAGAGCCCTTT 955

Oy 23 GluValLysLysTrpPheAlaValAlaLeuTrpAlaTrpAspIleValValAspAlaCys 42  
 Db 954 GAAGTGAAAAGCTGGATAGCAGTAGGCCCTCTGGCTGGATATTGTGTGATACTGT 895

Oy 43 AlaIleLysArgAsnHisIleMetAspLeucysIleLeucysGlnAlaAsnGlnAlaSer 62  
 Db 894 GCCATCTGAGAACCCATATTGGATTCATAGCTAACGCTAACGGGTCC 835

Oy 63 AlaThrSerGluGluCysThrValAlaTrpGlyIvaIcyAsnHisAlaPheHisPheHis 82  
 Db 834 GCTACTTCAGAGAGTGCTACTCTGCATGGCAAGTGTAACCATTGTTTCACTTCAC 775

Oy 83 CysIleSerArgTriPheLysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu 102  
 Db 774 TGCATCTCTGCTGGCTCAAACACGCCAGGTGTCATGGACAAAGGACTGGAA 715

Oy 103 PheGlnIby 105  
 Db 714 TTCCAAA 706

This Page Blank (uspto)

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 11, 2006 08:27:10 ; Search time 349 Seconds  
(without alignments)

Title: US-09-541-462B-2  
Perfect score: 616  
Sequence: 1 MAAMDVDTPSGTNSGAGKK.....KTRQVCPLDNREWEFQKYGH 108  
714.006 Million cell updates/sec

Scoring table: BLASTM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

```
-MOPSL=frame+_p2n model -DEV=1h
-Q=/abs/ABSSWEB/spool1/US09514162/runat_10032006_080737_22172/app_query.fasta_1
-DB=Published Applications NA_New -QFMT=FastA -SUFFIX=rnppn -MINMATCH=0.1
-LOOPCL=0 -LOOPBEXT=0 -UNITS=5tB -START=1 -END=-1 -MATRIX=BL09sum62
-TRANS=human.cdi -LIST=4 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFILE=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOSTSCORE=50h
-USER=US09514162@CGN_1_1_431 @runat_10032006_080737_22172 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=10 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

## Database :

```
Published Applications NA_New;*
1: /cgn2_6/podata/2/pubpna/us08_new_pub.seq;*
2: /cgn2_6/podata/2/pubpna/us06_new_pub.seq;*
3: /cgn2_6/podata/2/pubpna/us07_new_pub.seq;*
4: /cgn2_6/podata/2/pubpna/pct_new_pub.seq;*
5: /cgn2_6/podata/2/pubpna/us05_new_pub.seq;*
6: /cgn2_6/podata/2/pubpna/us09_new_pub.seq;*
7: /cgn2_6/podata/2/pubpna/us10_new_pub.seq;*
8: /cgn2_6/podata/2/pubpna/us10_new_pub.seq;*
9: /cgn2_6/podata/2/pubpna/us11_new_pub.seq;*
10: /cgn2_6/podata/2/pubpna/us11_new_pub.seq2;*
11: /cgn2_6/podata/2/pubpna/us11_new_pub.seq3;*
12: /cgn2_6/podata/2/pubpna/us11_new_pub.seq4;*
13: /cgn2_6/podata/2/pubpna/us60_new_pub.seq;*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	85.6	660	9	US-11-096-568A-11809 Sequence 11809, A
2	516.5	83.8	432	9	US-11-096-568A-14405 Sequence 26820, A
3	515.5	83.7	693	9	US-11-096-568A-26820 Sequence 28569, A
4	499	81.0	348	9	US-11-096-568A-28569 Sequence 28569, A

Sequence 78459, A  
Sequence 78459, A  
Sequence 2279, AP  
Sequence 2279, AP  
Sequence 554, APP  
Sequence 5740, AP  
Sequence 5740, AP  
Sequence 2098, AP  
Sequence 2098, AP  
Sequence 4, Appl  
Sequence 14, Appl  
Sequence 18, Appl  
Sequence 81177, A  
Sequence 81177, A  
Sequence 360, APP  
Sequence 6146, AP  
Sequence 6146, AP  
Sequence 459, APP  
Sequence 75906, A  
Sequence 75906, A  
Sequence 12921, A  
Sequence 3548, AP  
Sequence 1533, A  
Sequence 1239, AP  
Sequence 128, APP  
Sequence 16478, A  
Sequence 3705, AP  
Sequence 3994, AP  
Sequence 5433, AP  
Sequence 21222, A  
Sequence 132, APP  
Sequence 1680, AP  
Sequence 23080, A  
Sequence 730, APP  
Sequence 20676, A  
Sequence 150, APP  
Sequence 6605, AP  
Sequence 11058, A  
Sequence 39, APP  
US-11-096-568A-23080 Sequence 11096568A-730 Sequence 11096568A  
; Sequence 11809, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Theory  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096\_568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 11809 LENGTH: 660  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE: misc\_feature  
; NAME/KEY: misc\_feature  
; LOCATION: (1)\_(660)  
; OTHER INFORMATION: Ceres Seq. ID no. 13657464  
US-11-096-568A-11809

Alignment Scores:  
Pred. No.: 1.97e-49  
Score: 527.00  
Percent Similarity: 79.8%  
Best Local Similarity: 75.8%  
Query Match: 85.6%

Length: 660  
Matches: 94  
Conservative: 5  
Mismatches: 7  
Indels: 18











APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
 i APPLICANT: Ducleit, Aymeric  
 i APPLICANT: Bouquelier, Lydie  
 i APPLICANT: Jobert, Severin  
 i APPLICANT: Cluseel, Catherine  
 TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
 FILE REFERENCE: 56.USA.CIP  
 CURRENT APPLICATION NUMBER: US/09/978,360A  
 CURRENT FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: US 60/066,677  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: US 60/069,957  
 PRIOR FILING DATE: 1997-12-17  
 PRIOR APPLICATION NUMBER: US 60/074,121  
 PRIOR FILING DATE: 1998-02-09  
 PRIOR APPLICATION NUMBER: US 60/081,563  
 PRIOR FILING DATE: 1998-04-13  
 PRIOR APPLICATION NUMBER: US 60/096,116  
 PRIOR FILING DATE: 1998-08-10  
 PRIOR APPLICATION NUMBER: US 60/099,273  
 PRIOR FILING DATE: -09-04  
 PRIOR APPLICATION NUMBER: US 09/191,997  
 PRIOR FILING DATE: 1998-11-13  
 PRIOR APPLICATION NUMBER: US 09/215,435  
 PRIOR FILING DATE: 1998-12-17  
 PRIOR APPLICATION NUMBER: PCT/IB98/02122  
 PRIOR FILING DATE: 1998-12-17  
 PRIOR APPLICATION NUMBER: US 09/247,155  
 PRIOR FILING DATE: 1999-02-09  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 810  
 SOFTWARE: Patent.pml  
 SEQ ID NO 4  
 LENGTH: 648  
 TYPE: DNA  
 ORGANISM: Homo Sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 187..438  
 FEATURE:  
 NAME/KEY: polyA\_signal  
 LOCATION: 612..617  
 FEATURE:  
 NAME/KEY: polyA\_site  
 LOCATION: 632..648  
 US-09-978-360A-4  
 Alignment Scores:  
 Pred. No.: 1.06e-14 Length: 648  
 Score: 217.00 Matches: 43  
 Percent Similarity: 44.5% Conservative: 18  
 Best Local Similarity: 31.4% Mismatches: 40  
 Query Match: 35.2% Indels: 3  
 DB: 5  
 US-09-541-462B-2 (1-108) x US-09-978-360A-4 (1-648)  
 QY 2 AlaAlaAlaLysAspValApthrProSglyThrAsnSerGlyAlaGlyLysIsg 21  
 DB 49 GCGGCACATGGTCCTTTATACTTCCGGGCTGCCAACGGAAGC 108  
 QY 22 PheGlu------23  
 DB 109 GCGGAGCAAACTGGCTGTCATGTTGCAAGCCATTGTGAGATATCCCA 168  
 QY 24 -----ValLysLysTrpAsnAlaValAlaLeutrp 33  
 DB 169 ACGTGAGGCTCTGCTGTCATGAAGGTGAAGATTAACTGCTGAAACCTCG 228  
 QY 34 AlaTPAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuYtf 53  
 DB 229 CTCCTGGCAACCATGAGAACTGTCATCTCAGGATTAACGGATGTC 288

Qy 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73  
 Db 289 CCTGACTGCAAG-----GTCGGCGGACACTCCGCTGGTGGGGCGC 333

Qy 74 ValCysAsnHisAlaPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93  
 Db 334 CAGTGCTCCACACTGCTTCACATGATTGATCTCAAGTGGCTCACGCACAGGGT 393

Qy 94 -----CysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107  
 Db 394 CAGCAGCACTOCCCCATGAGCCAGGAATGGAACTGAGGTTCAAGGAGTGGGCC 444

RESULT 15  
 US-11-057-484A-14  
 Sequence 14, Application US/11057484A  
 GENERAL INFORMATION:  
 / PUBLICATION NO. US20060029331A1  
 / APPLICANT: Finkel, Terri H.  
 / APPLICANT: Yin, Jiyi  
 / TITLE OF INVENTION: Cellular Genes Regulated by HIV-1  
 / TITLE OF INVENTION: Infection and Methods of Use Thereof  
 / FILE REFERENCE: CHOP\_0146CIP  
 / CURRENT APPLICATION NUMBER: US/11/057,484A  
 / CURRENT FILING DATE: 2005-02-14  
 / PRIOR APPLICATION NUMBER: US 10/368,803  
 / PRIOR FILING DATE: 2003-02-19  
 / PRIOR APPLICATION NUMBER: US 60/358,495  
 / PRIOR FILING DATE: 2002-02-19  
 / NUMBER OF SEQ ID NOS: 25  
 / SOFTWARE: FastSEQ for Windows Version 3.0  
 / SEQ ID NO 14  
 / LENGTH: 450  
 / TYPE: DNA  
 / ORGANISM: Homo sapien  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / LOCATION: (0)..(0)  
 / OTHER INFORMATION: n = A, C, G or T  
 US-11-057-484A-14

Alignment Scores:  
 Pred. No.: 1.15e-14 Length: 450  
 Score: 215.00 Matches: 41  
 Percent Similarity: 53.6% Conservative: 11  
 Best Local Similarity: 42.3% Mismatches: 23  
 Query Match: 34.9% Indels: 23  
 DB: 9 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-057-484A-14 (1-450)  
 Qy 11 SerGlyThrAsnSerGlyAlaGlyLysIsgTheGluValBlysLysTrpAsnAlaVal 30  
 Db 54 TCAGGCTCCAAAGTGGGA--GGGACAAGATGTTCTCCCTCAAGAAGTGGAAACGGGTG 110  
 Qy 31 AlaLeutrpAlaLysAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50  
 Db 111 GCCTGTGAGCTGGACTGGATACGGCCTCAGCTCAGGT-----160

Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70  
 Db 161 -----CCAGTC 166

Qy 71 AlaTrpGlyValCysAsnHisAlaPheHisIshisCysIleSerArgTrpLeuYtfThr 90  
 Db 167 GTCTGGGAGAATTAATCATTCCTCCAACTGCTGATGTCCTGTGGTAAACAG 226

Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107  
 Db 227 AACATGNTGCCTCTCGCCACAGCTGGTGTCAAAGAAATCGC 277



GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame\_plus\_B2n model

Run on: March 11, 2006, 08:13:49 ; Search time 134 Seconds

(without alignments)

1432.662 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616

Sequence: 1 MAAMDVDTPTSGTNSGAGK... KTRQVCPLDNREWFKQYGH 108

Scoring table: BLASTIN62

Xgapext 10.0 , Ygapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delect 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
 -MODE=frame\_plus\_model -DEV=xlh  
 -O=/abs/ASSWEB/spool/US09541462/runat\_10032006\_080729\_220008/app\_query.fasta\_1  
 -DB=1-issued\_patents\_NA -QFMT=fasta -SUFFIX=xrn1 -MINMATCH=0.1 -LOOPCL=0  
 -LIST=45 -DOCALIGN=200 -THR SCORE=poct -END=1 -MATRIX=blosum62 -TRANS=human10.cdi  
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MAXLEN=0 -ALIGN=15  
 -HOST=USER=US09541462 @runat\_10032006\_080729\_220008  
 -DBTIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXTH=7

Database : Issued\_Patents\_NA:\*

1: /cgns\_6/\_ptodata/1/in/1/COMB.seq:\*

2: /cgns\_6/\_ptodata/1/in/5/COMB.seq:\*

3: /cgns\_6/\_ptodata/1/in/6A/COMB.seq:\*

4: /cgns\_6/\_ptodata/1/in/6B/COMB.seq:\*

5: /cgns\_6/\_ptodata/1/in/H/COMB.seq:\*

6: /cgns\_6/\_ptodata/1/in/PCTUS.COMB.seq:\*

7: /cgns\_6/\_ptodata/1/in/PP/COMB.seq:\*

8: /cgns\_6/\_ptodata/1/in/RE/COMB.seq:\*

9: /cgns\_6/\_ptodata/1/in/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	
1	616	100.0	482	3	US-09-513-999C-3894	Sequence 3894, Ap	
2	616	100.0	504	3	US-09-944-322A-5	Sequence 5, Appli	
3	616	100.0	507	3	US-09-949-016-4940	Sequence 4940, Ap	
4	616	100.0	508	3	US-09-913-324A-3	Sequence 3, Appli	
5	501.5	81.4	3208	3	US-09-780-016-27	Sequence 27, Appli	
6	501.5	81.4	3208	3	US-10-214-811-27	Sequence 27, Appli	
7	501.5	81.4	3208	3	US-10-766-074-27	Sequence 1731, Appli	
8	400.5	479	77.8	411	3	US-09-640-211A-1731	Sequence 1731, Ap
c	400.5	65.0	490	3	US-09-270-767-26812	Sequence 26812, A	

Sequence 11265, A	US-09-270-767-11265
Sequence 10370, A	US-09-513-999C-10371
Sequence 15180, A	US-09-621-970-15180
Sequence 4, Appli	US-09-914-344A-4
Sequence 5495, Ap	US-09-248-796A-5495
Sequence 7, Appli	US-09-846-312A-7
Sequence 7, Appli	US-09-542-497A-7
Sequence 7, Appli	US-10-108-767-7
Sequence 492, App	US-09-313-29A-492
Sequence 27, Appli	US-09-509-360B-27
Sequence 1817, Ap	US-09-621-976-1817
Sequence 1854, Ap	US-09-621-976-1854
Sequence 2051, Ap	US-09-521-976-2051
Sequence 1945, Ap	US-09-621-976-1945
Sequence 16682, A	US-09-949-016-16682
Sequence 27, Appli	US-09-720-757-10788
Sequence 10788, A	US-09-799-451-296
Sequence 26253, Ap	US-09-270-767-26253
Sequence 459, Ap	US-10-0104-047-459
Sequence 667, Ap	US-09-655-667
Sequence 10, Appli	US-09-928-303-10
Sequence 304, Ap	US-09-774-528-304
Sequence 304, Ap	US-10-120-988-304
Sequence 4980, Ap	US-09-949-016-4980
Sequence 2, Appli	US-09-928-303-2
Sequence 255, Ap	US-09-774-528-255
Sequence 255, Ap	US-10-120-988-255
Sequence 1, Appli	US-07-945-283-1
Sequence 763, Ap	US-09-799-451-763
Sequence 1680, Ap	US-10-104-047-1680
Sequence 1319, Ap	US-09-640-211A-1319
Sequence 378, Ap	US-09-949-016-378
Sequence 2914, Ap	US-09-949-016-2914
Sequence 220, Ap	US-09-799-451-220
Sequence 20, Appli	US-09-923-655-20
Sequence 3134, Ap	US-09-949-016-3134

#### ALIGNMENTS

RESULT 1  
 US-09-513-999C-3894  
 Sequence 3894, Application US/09513999C

/ GENERAL INFORMATION:  
 / APPLICANT: Dumas Milne Edwards, J.B.  
 / APPLICANT: Ducldart, A.  
 / APPLICANT: Giordano, J.Y.  
 / TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 / Patent No. 6783961  
 / FILE REFERENCE: 59.US2.REG  
 / CURRENT APPLICATION NUMBER: US/09-513-999C  
 / CURRENT FILING DATE: 2000-02-24  
 / PRIOR APPLICATION NUMBER: US 60/1122,487  
 / PRIOR FILING DATE: 1999-02-26  
 / NUMBER OF SEQ ID NOS: 36681  
 / SOFTWARE: Patent, pm  
 / SEQ ID NO 3894  
 / LENGTH: 482  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: 29..352

Alignment Scores:  
 Pred. No.: 1.48e-66 Length: 482  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-513-99C-3894 (1-482)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysIys 20  
 Db 29 ATGGCCGACCGATGTGAATGGCTTGGATTCGGCTTGAGATGGAG 88

Qy 21 ArgPheGluValLysLysTrpAsnAlaValLeuTrpAspIleValValAsp 40  
 Db 89 CGCTTGAACTGAAAGTGAAATGGCTTGGATTCGGCTTGAGATGGTGTAT 148

Qy 41 AsnCysAlaLalleCysArgArgAnHiSleMetAspIleGluCysGlnAlaAsnGin 60  
 Db 149 AACCTGGCATCTGGAGAACCAATTARGATCTTGCATAGATGTAAAGCTAACAG 208

Qy 61 AlaSerAlaThrSerGluCysThrValAlaLysTrpGlyAlaCysAsnHisAlaPheHis 80  
 Db 209 GCGTCCGCTACTCTGAAAGTGTACTGTCGCTGGAGCTGTAAACCATGCTTTAC 268

Qy 81 PheHisCysteSerArgTrpLeuLysThrArgGlnValCysProLeuAspIleArgGlu 100  
 Db 269 TTCCACTGCACTCTGCTGGCTCAAACAGCACGGTGTCCATTGACAAGAG 328

Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 329 TGGGAATCCAAAAGTAGTGGCAC 352

RESULT 2

US-09-914-324A-5  
 i Sequence 5, Application US/0914324A  
 i Patent No. 6858709  
 i GENERAL INFORMATION:  
 i APPLICANT: Conway, Joan A.  
 i APPLICANT: Conway, Ronald C.  
 i APPLICANT: Kamura, Takumi  
 i APPLICANT: Oklahoma Medical Research Foundation  
 i TITLE OF INVENTION: No. 65587031 Component of von Hippel-Lindau Tumor Suppressor  
 i FILE REFERENCE: 021044-004600US  
 i CURRENT APPLICATION NUMBER: US/09/914,324A  
 i PRIORITY FILING DATE: 2003-02-11  
 i PRIORITY APPLICATION NUMBER: US 60/121,787  
 i PRIORITY APPLICATION NUMBER: WO PCT/US00/04838  
 i PRIORITY FILING DATE: 2000-02-25  
 i SOFTWARE: PatentIn Ver. 2.1  
 i SEQ ID NO 5  
 i LENGTH: 504  
 i TYPE: DNA  
 i ORGANISM: Mus sp.  
 i FEATURE: CDS  
 i NAME/KEY: CDS  
 i LOCATION: (18)..(344)  
 i OTHER INFORMATION: Rbx1  
 i US-09-914-324A-5

Alignment Scores:  
 Pred. No.: 1.57e-66 Length: 504  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Mismatches: 0  
 Best Local Similarity: 100.0% Indels: 0  
 Query Match: 100.0% Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-016-4940 (1-507)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysIys 20  
 Db 7 ATGGCGACGGATGGATGGCTACCCGAGGCCACGCGCCCTCTGGATTCGGATGGAG 66

Qy 21 ArgPheGluValLysLysTrpAsnAlaValLeuTrpAspIleValValAsp 40  
 Db 67 CGCTTGAACTGAAAGTGGATTCGGATGGCTCTGGATTCGGATGGTGTAT 126

Qy 41 AsnCysAlaLalleCysArgAsnHisIleMetAspIleGluCysGlnAlaAsnGin 60  
 Db 127 AACCTGGCATCTGGAGAACCAATTATGGATCTTGCATAGATGTCAAGCTAACAG 186

Qy 61 AlasSerAlaThrSerGluGlucysThrValAlaTrpCysLysAlaAsnHisAlaPheHis 80  
 Db 187 GCTGCCCTACTTCAGAGTGTACTGTCATGGAGCTGTAAACATGCTTTAC 246

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 247 TTCCACTGCACTCTCTGGTCALAAACACAGACAGTGTCATTGGACAACAGAG 306

Qy 101 TrpGluPheGlnLysTyrGlyHis 108  
 Db 307 TGGAAATCCAAAATGATGGGCAC 330

RESULT 4  
 Sequence 3, Application US/0914324A  
 Patent No. 688709  
 GENERAL INFORMATION:  
 APPLICANT: Conway, Joan A.  
 APPLICANT: Conway, Joan A.  
 APPLICANT: Kamara, Takumi  
 APPLICANT: Oklamoma Medical Research Foundation  
 TITLE OF INVENTION: No. 688709-1 Component of von Hippel-Lindau Tumor Suppressor  
 FILE REFERENCE: 021044-004600US  
 CURRENT FILING DATE: 2003-02-11  
 PRIORITY APPLICATION NUMBER: US 60/121,787  
 PRIORITY FILING DATE: 1999-02-26  
 PRIORITY APPLICATION NUMBER: WO PCT/US00/04838  
 PRIORITY FILING DATE: 2000-02-25  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 508  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (7) .. (333)  
 OTHER INFORMATION: Rbx1  
 US-09-914-324A-3

Alignment Scores:  
 Pred. No.: 1.58e-66 Length: 508  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 3 0 Gaps: 0

US-09-541-462B-2 (1-108) × US-09-780-016-27 (1-3208)

Qy 16 GlyAlaGlyLysLysArgPheGluValLysSASPAlaValAlaLeuTrpAlaTrp 35  
 Db 2752 GGAGCATAAAAAAA-----AAAAAATGAATGCAAGCCCTCTGGCCCTGG 2802

Qy 36 AspIleValValAspAsnCysAlaIleCysSArgAsnHistLeMetAspLeuCysIleGlu 55  
 Db 2803 GATATTGTTGATACTGTGCATCTGAGAACCATTTGATCTTGATAGAA 2862

Qy 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGlyCysThrValAlaTrpGlyValCys 75  
 Db 2863 TGTCAGCTAACCGGCGTCGTACTGCAAGGAGTGTACTGTGCAATGGGAGCTGT 2922

Qy 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysPro 95  
 Db 2923 AACATGCTTTCTACTTCCACTGTGATCTCGCTGGCTAAACAGACAGGTGTGCCA 2982

Qy 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108  
 Db 2983 TTGGACAACGAGGTGGAAATTCAAAGTAGGGCAC 3021

RESULT 6  
 US-10-214-811-27  
 Sequence 27, Application US/10214811  
 Patent No. 674321  
 GENERAL INFORMATION:  
 APPLICANT: Donoho, Gregory  
 APPLICANT: Scoville, John  
 APPLICANT: Turner, C. Alexander Jr.  
 APPLICANT: Friedrich, Glenn  
 APPLICANT: Abuin, Alejandro  
 APPLICANT: Zambrowicz, Brian  
 APPLICANT: Sands, Arthur T.  
 TITLE OF INVENTION: No. 6709456el Human Proteases and

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 7 ATGGCCGACGGATGCGATGTCGATACCCGAGCGACCAACAGGGGGCAAGAG 66

Qy 21 ArgPheGluValLysSASPAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
 Db 67 CGCTTGAACTGAAAGTGAATGAGTCAGCCCTGGGCTGGATATTGTCGTTGAT 126

Qy 41 AsnCysAlaIleCysArgAsnHistLeMetAspLeuCystIleGluCysGlnAlaAsnGin 60  
 Db 127 AACTGCCATCTGCAAGAACCATTTGCTAGATGTCAGCTAACCG 186

Qy 61 AlasSerAlaThrSerGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 187 GCGTCGCTACTTCAGAGTGTACTGTCGATCGGACTCTGTAACCATGCTTTAC 246

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 247 TTCCACTGCACTCTCGCTGGCTCAAACAGCAAGGTGTCCATTGGACAACAGAG 306

Qy 101 TrpGluPheGlnLysTyrGlyHis 108

TITLE OF INVENTION: Polynucleotides Encoding the Same  
FILE REFERENCE: LEX-0132-USA  
CURRENT APPLICATION NUMBER: US/10/214,811  
CURRENT FILING DATE: 2002-08-07  
PRIOR APPLICATION NUMBER: US/09/780,016  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US/10/214,816  
PRIOR FILING DATE: 2001-02-11  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 27  
LENGTH: 3208

TYPE: DNA  
ORGANISM: homo sapiens  
US-10-214-811-27

Alignment Scores:  
Pred. No.: 2.1e-51 Length: 3208  
Score: 501.50 Matches: 88  
Percent Similarity: 95.7% Conservative: 1  
Best Local Similarity: 94.6%  
Query Match: 81.4%  
DB: 3

US-09-541-462B-2 (1-108) x US-10-766-074-27 (1-3208)

Qy 16 GlyAlaGlyLysArgPheGluValLysLystrpAsnAlaValAlaLeuTrpAlaTrp 35  
Db 2752 GGACATAAAAAAA----AAAAATGGATGCACTAGCCTCTGGCCGG 2802

Qy 16 GlyAlaGlyLysArgPheGluValLysLystrpAsnAlaValAlaLeuTrpAlaTrp 35  
Db 2752 GGACATAAAAAAA----AAAAATGGATGCACTAGCCTCTGGCCGG 2802

Qy 36 AspIleValValAspIleCysAlaIleCysA9AsnHisIleMetAspLeuCysIleIeu 55  
Db 2803 GATTTGGTGTCAATTACTGCACTTCGCAACCATTTATGGATCTTGATGAA 2862

Qy 56 CysGlnAlaAsnGlnAlaserAlaThrSerGluGlycylvalAlaTrpGlycylvalCys 75  
Db 2863 TGAAGCTAACGGCTCGTACTCAGAAGTCAGTAGCCCTCTGGCTGG 2922

Qy 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpIleLysThrArgClnValCysPro 95  
Db 2923 AACATGCTTTCACTTCACCTGCATCTCGTGGCTCAAACAGACAGGGTGTCCA 2982

Qy 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108  
Db 2983 TTGCACACAGAGGTGGGAAATTCCAAAGTAATGGCAC 3021

RESULT 8  
US-09-640-211A-1731  
Sequence 1731, Application US/09640211A  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shank, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Modification of Gene Transcription  
; FILE REFERENCE: 11000.1021CU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 1731  
; LENGTH: 411

TYPE: DNA  
ORGANISM: Pinus radiata  
FEATURE:  
NAME KEY: misc feature  
LOCATION: (1)..(411)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-640-211A-1731

Alignment Scores:  
Pred. No.: 7.79e-50 Length: 411  
Score: 479.00 Matches: 90  
Percent Similarity: 85.0% Conservative: 6  
Best Local Similarity: 79.6%  
Query Match: 77.8%  
DB: 3

US-09-541-462B-2 (1-108) x US-09-640-211A-1731 (1-411)

Qy 3 AlaAlaMetAspValAsp-----ThrProSer-----GlyThrAsnSerGlyAla 17  
Db 74 GCTCAACAGACATAAGATGATGATTCCCGTGGCAGGGTCTCCAAAGCG 133

RESULT 10  
 US-09-270-767-11265/c  
 Sequence 11265, Application US/09270767  
 Patent No. 6703491  
 GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270, 767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 11265  
 ; LENGTH: 1101  
 ; TYPE: DNA  
 ; ORGANISM: *Drosophila melanogaster*  
 ; US-09-270-767-11265

QY 18 Gly-----LysLysArgPheGluValLysLeuTrpAsnAlaVal 30  
 DB 134 GGCAAGGGCTTCCACCAAAGGCCAACGTTGAAATCAGAAGTCGTGA 193

QY 31 AlaLeuTrpAlaTrpAspIleValAspAsnCysAlaLeuCysArgAsnHisIleMet 50  
 DB 194 GCCCTTGCGTGGATAATTGCTGTTATAATTGCAATTGCAATTCAGAAACATCATG 253

QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaserAlaThrSerGluGluCysThrVal 70  
 DB 254 GACCTCTGATTGAGTCAGGAAATCAGCAACTGAAATGFACTGTT 313

QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90  
 DB 314 GCATGGGTGTTGCATTCAGCCTTCAATTGATAAATGCTGGCTCAAGACA 373

QY 91 ArgGlnValCysProLeuAspAspArg-GlutTrpGlu 102  
 DB 374 CGAACAGGTGCCATTAGATAATAAGTCAGTGGGAG 410

RESULT 9  
 US-09-270-767-26812/c  
 ; Sequence 26812, Application US/09270767  
 ; Patent No. 6703491  
 GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 26812  
 ; LENGTH: 490  
 ; TYPE: DNA  
 ; ORGANISM: *Drosophila melanogaster*  
 ; US-09-270-767-26812

Alignment Scores:  
 Pred. No.: 5 MetAspValAspThrProSerGlyThrAsnSerGly-----AlaGlyLysLys 20  
 Score: 1.25e-39  
 Percent Similarity: 400 50  
 Best Local Similarity: 77.6%  
 Query Match: 13  
 DB: 981 ATGGACTTCATGAGGAAAGCCATCTGTAGGGAGCTGTCAAGGACGGAG 92

US-09-541-462B-2 (1-108) x US-09-270-767-11265 (1-1101)  
 QY 5 MetAspValAspThrProSerGlyThrAsnSerGly-----AlaGlyLysLys 20  
 Db 981 ATGGACTTCATGAGGAAAGCCATCTGTAGGGAGCTGTCAAGGACGGAG 92

QY 21 ArgPheGluValLysLysIleStpAsnAlaValAlaLeuTrpAspIleValAsp 40  
 Db 921 CGCTTGTGCTGTAAGAAATGGTGCAGCACTGTGGGATGGACTAGTGGAC 86

QY 41 AsnCysValAlleCysArgAsnHisIleMetAspIleuCysIleGluCysGlnAlaLysGln 60  
 Db 861 AACCTGTGCCATTCGGTAAACCACATCATGAACTGTGATCGAGTGGGGAC--- 80

QY 61 AlaSerAlaThrSerGluCysIleSerGlyValAlaLeuTrpGlyValCysAsnHisAlaPheHis 80  
 Db 804 CCGATGAAACCAAGACCAAGTGGACTGGGCTGGGCAACCAAGCATCCAT 74

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 744 TACCACTGATGGCGCTGGTAAACCGCTGGTCCCTGGACAAACAGGAG 68

QY 101 TrpGluPheGlnLysTrpGly 107  
 Db 684 TGGGTCTACCAAGAGTACGGC 664

RESULT 11  
 US-09-541-462B-2 (1-108) x US-09-270-767-26812 (1-490)  
 QY 5 MetAspValAspThrProSerGlyThrAsnSerGly-----AlaGlyLysLys 20  
 DB 370 ATGACTCTAAATGAGAAAGGCCATCCGTAGTGGAGAGTCAGACGGAG 311

QY 21 ArgPheGluValLysIleTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
 DB 310 CGCTTGTGCTGAGAAATGGGTGCGCACGCGCATGCGGATGGAGCTGAGTGGAC 251

QY 41 AspCysValAlleCysArgAsnHisIleMetAspIleuCysIleGluCysGlnAlaLysGln 60  
 DB 250 AACCTGTGCCATTCGGTAAACCAAGTGGACTGGGCTGGACATGGGGAC--- 194

QY 61 AlaserAlaThrSerGluCysIleThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 DB 193 CGGAATGAAACCAAGACCAAGTGCACGTCGCTGGGGAGTCACACGGCATTCAT 134

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 DB 133 TACCACTGATCCGGCTGGTGAAGACGGCCTGTCGGTGAACAAAGGAG 74

QY 101 TrpGluPheGlnLysTrpGly 107  
 DB 73 TGCTGCTACCAAGAGTACGGC 53

```

FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 20
; OTHER INFORMATION: k=g or t
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 38
; OTHER INFORMATION: s=g or c
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 79
; OTHER INFORMATION: n=a, g, c or t
US-09-513-99C-10371

Alignment Scores:
Pred. No.: 2.05e-39 Length: 402 Score: 394.00 Matches: 76 Percent Similarity: 73.1% Mismatches: 2 Best Local Similarity: 73.1% Indels: 64.0% Query Match: 3 DB: 102

US-09-541-462B-2 (1-108) x US-09-621-976-15180 (1-463)
; MetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysArgPheGluVal 5
QY 35 ATGGATGTGGATAACCGAGGCCAAACA GCGCAGCAAGAAGGCTTGAAGTG 94
Db 35 ATGGATGTGGATAACCGAGGCCAAACA GCGCAGCAAGAAGGCTTGAAGTG 94
; LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaLe 44
QY 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaLe 44
Db 95 AAAAGGC----- 102
; 95 AAAAGGC-----

US-09-541-462B-2 (1-108) x US-09-621-976-15180 (1-463)
; 95 AAAAGGC----- 102
Db 95 AAAAGGC----- 102

QY 45 CysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64
Db 103 - ----- 103
; -ATAGAATCTCAAGCTAACCGGTCCCGTACT 135
Db 65 SerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIle 84
Db 136 TCAGAGAGGTACGTGCAATTGGAGATGGGAGTGTGAACTTCACTTCACTGCACT 195
; 136 TCAGAGAGGTACGTGCAATTGGAGATGGGAGTGTGAACTTCACTTCACTGCACT 195
Db 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104
Db 196 TCTCCCTGGCTCAAACACCAAGCTGGCATATTGGACAAACAGAGTGGAAATTCCA 255
; 196 TCTCCCTGGCTCAAACACCAAGCTGGCATATTGGACAAACAGAGTGGAAATTCCA 255
Db 105 LysTrpGlyHis 108
Db 256 AGATATGGGCAC 267
; RESULT 13
US-09-914-324A-4
; sequence 4, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conway, Joan A.
; APPLICANT: Conway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: Non-helical Component of von Hippel-Lindau Tumor Suppressor
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914_324A
; PRIOR APPLICATION NUMBER: US/09/914_324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Stachyromyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(369)
; OTHER INFORMATION: Rx1
US-09-914-324A-4

Alignment Scores:
Pred. No.: 3.3e-38 Length: 480 Score: 385.00 Matches: 64 Percent Similarity: 65.5% Mismatches: 10 Best Local Similarity: 56.6% Indels: 29 Query Match: 3 DB: 1

US-09-541-462B-2 (1-108) x US-09-914-324A-4 (1-480)
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 74
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15180
; Sequence 15180, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Robert S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SEQ ID NO 15180
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 74
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15180

```

5 MetAspPvalAspThrProSerGlyThrAsnSerGlyAlaGly----- 18  
 25 ATGGATGTGATGAAGTGAATCGCAAAAATTGGCAAAGTCAAACCAAGTGGCCA 84

Qy 19 -----LysLysArgPheGluValLysLysSerThrAsnAlaValAlaLeuTrpAla 34  
 Db 85 GTGGAAACCAAAAGAGAGATTGAAATTAGAAATTGACCTTCGCTCA 144

Qy 35 TrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIle 54  
 Db 145 TCGGATTTAGCTGTGCAACTGTGCTATTGAGAACCATTCATGAACTGCATT 204

Qy 55 GluCysGlnAlaAsnGlnAlaSerAlaThrSerGluCysThrValAlaItpGlyVal 74  
 Db 205 GAATGCCAGCCAAAGCCATGAGGCCATGAGGCCATGAGCTGGCTGTC 264

Qy 75 CysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCys 94  
 Db 265 TGTAAATACGCTTCCATTGCACTGATTATAAATGGATCAAGAACAGACCGATGCG 324

Qy 95 ProLeuAspAsnArgGluItpGluPheGlnLysTrpGly 107  
 Db 325 CCATAGATAACCAACCTTGSCAGTTAGCAAGATGCGGT 363

RESULT 14  
 US-09-248-796A-5495  
 ; Sequence 5495, Application US/09248795A  
 ; Patent No. 6747137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keith Weinstock et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
 ; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS  
 ; CURRENT APPLICATION NUMBER: US/09/248,796A  
 ; CURRENT FILING DATE: 1999-02-12  
 ; PRIOR APPLICATION NUMBER: US 60/074,725  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 60/096,409  
 ; PRIOR FILING DATE: 1998-08-13  
 ; SEQ ID NO: 28208  
 ; LENGTH: 357  
 ; TYPE: DNA  
 ; ORGANISM: Candida albicans  
 ; US-09-248-796A-5495

Alignment Scores:  
 Pred. No.: 3.26e-37 Length: 357  
 Score: 375.50 Matches: 62  
 Percent Similarity: 73.3% Conservative: 12  
 Best Local Similarity: 61.4% Mismatches: 26  
 Query Match: 61.0% Indels: 1  
 DB: 3 Gaps: 1

US-09-541-462B-2 (1-108) × US-09-248-796A-5495 (1-357)  
 Qy 9 ThrProSerGlyThrAsnSerGlyAlaGlyLysLysSerGluValLysLysTrpAsn 28  
 Db 52 ACAACGGAAACAACTAAACCATCATCAAAACCAGATTGAGTGAATAATTGGACA 111

Qy 29 AlaValAlaLeuTrpIleValAspAsnCysAlaIleCysArgAsnHis 48  
 Db 112 GCGTAGCTGGTTGGCATGGGATATGCAAAATTGAAATTGCAATTCTGAAATCAT 171

Qy 49 IleMetAspLeuCysIleGluCysGlnAlaAsn--GlnAlaSerAlaThrSerGluGlu 67  
 Db 172 TTAAUTGGAAACATGPAATGTAATGTCACCAAAATGCTATGGGTAAATTCTTCAGAAAG 231

Qy 68 CysThrIleValAlaItpGlyValCysAsnHisAlaIleCysSerHisCysIleSerArgTrp 87  
 Db 232 TGTATTCCTGCTTGGGAATGATGATCATGCATTCAATTACATTGATTAGAGATGG 291

Qy 88 LeuIlysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107

US-09-248-796A-5495  
 ; Sequence 5495, Application US/09248795A  
 ; Patent No. 6747137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rigel Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: Ubiquitin Ligase Assay  
 ; FILE REFERENCE: 02104-007010US  
 ; CURRENT APPLICATION NUMBER: US/09/826,312A  
 ; CURRENT FILING DATE: 2001-04-03  
 ; PRIORITY APPLICATION NUMBER: US 09/542,497  
 ; PRIORITY FILING DATE: 2000-04-03  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 7  
 ; LENGTH: 342  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: RING finger protein ROC2  
 ; US-09-826-312A-7

Alignment Scores:  
 Pred. No.: 2.24e-26 Length: 342  
 Score: 287.00 Matches: 48  
 Percent Similarity: 63.9% Conservative: 14  
 Best Local Similarity: 49.5% Mismatches: 31  
 Query Match: 46.6% Indels: 4  
 DB: 3 Gaps: 2

US-09-541-462B-2 (1-108) × US-09-826-312A-7 (1-342)

Qy 11 SerGlyThrAsnSerGlyAlaGlyLysLysSerGluValLysLysTrpAsnAlaVal 30  
 Db 58 TCAGGCTCAACGTGGAA---GGGACACAGATGCTCCCTCAAGAACCTGGTG 114

Qy 31 AlaLeutItpPalalrAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50  
 Db 115 GCAATGTTGAGCTGGGACGTTGAGTGCCTACATGAGGGTCCAGGTGATG 174

Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70  
 Db 175 GATGCTGTTAGATGTCAGCTAACGCTAAAC-----AAACAGAGGACTGTTGTTGTC 225

Qy 71 AlaItpGlyValCysAsnHisAlaPheHisPheIleSerArgTrpLeuIleThr 90  
 Db 226 GTCCTGGGGAAATGTAATCTTCCATCAACTGCTGATGTCCTGTTGAAACAG 285

Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107  
 Db 286 AACAAATCGTGCCTCTGCAAGGGTGGTGTGAAAGATCGGC 336

Search completed: March 11, 2006, 08:22:43  
 Job time : 137 secs

This Page Blank (uspto)

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 14:30:51 ; Search time 297.184 Seconds

(without alignments)

2538.786 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1 atggccggcggatggatgt.....tccaaaatgtggcactag 3.27

Scoring table: OLIGO\_NJUC

Gapop\_60.0 , Gapext 60.0

Searched: 7673375 seqs, 1153648444 residues

Word size : 12

Total number of hits satisfying chosen parameters: 38280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

#### Post-processing: Listing first 45 summaries

Database : Published Applications NA\_New:\*

```
1: /cgns_6/ptodata/2/pubnpna/us09_NEW_PUB.seq;*
2: /cgns_6/ptodata/2/pubnpna/us06_NEW_PUB.seq;*
3: /cgns_6/ptodata/2/pubnpna/us07_NEW_PUB.seq;*
4: /cgns_6/ptodata/2/pubnpna/PCT_NEW_PUB.seq;*
5: /cgns_6/ptodata/2/pubnpna/us05_NEW_PUB.seq;*
6: /cgns_6/ptodata/2/pubnpna/us09_NEW_PUB.seq;*
7: /cgns_6/ptodata/2/pubnpna/us10_NEW_PUB.seq;*
8: /cgns_6/ptodata/2/pubnpna/us11_NEW_PUB.seq;*
9: /cgns_6/ptodata/2/pubnpna/us11_NEW_PUB.seq;*
10: /cgns_6/ptodata/2/pubnpna/us11_NEW_PUB.seq2;*
11: /cgns_6/ptodata/2/pubnpna/us11_NEW_PUB.seq3;*
12: /cgns_6/ptodata/2/pubnpna/us11_NEW_PUB.seq4;*
13: /cgns_6/ptodata/2/pubnpna/us06_NEW_PUB.seq;*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	25	7.6	25	12	US-11-121-849-188861 Sequence 188861,
2	25	7.6	25	12	US-11-121-849-188862 Sequence 188862,
3	25	7.6	25	12	US-11-121-849-188863 Sequence 188863,
4	25	7.6	25	12	US-11-121-849-188864 Sequence 188864,
5	25	7.6	25	12	US-11-121-849-188865 Sequence 188865,
6	25	7.6	25	12	US-11-121-849-188866 Sequence 188866,
7	25	7.6	23	12	US-11-121-849-188867 Sequence 188867,
8	23	7.0	23	12	US-11-121-849-188868 Sequence 188868,
9	19	5.8	19	10	US-11-101-244-692822 Sequence 692822,
10	19	5.8	19	10	US-11-101-244-692823 Sequence 692823,
11	19	5.8	19	10	US-11-101-244-692824 Sequence 692824,
12	19	5.8	19	10	US-11-101-244-692825 Sequence 692825,
13	19	5.8	19	10	US-11-101-244-692826 Sequence 692826,
14	19	5.8	19	10	US-11-101-244-692827 Sequence 692827,
15	19	5.8	19	10	US-11-101-244-692828 Sequence 692828,
16	19	5.8	19	10	US-11-101-244-692829 Sequence 692829,
17	19	5.8	19	10	US-11-101-244-692830 Sequence 692830,
18	19	5.8	19	10	US-11-101-244-692831 Sequence 692831,
19	19	5.8	19	10	US-11-101-244-692832 Sequence 692832,
20	19	5.8	19	10	US-11-101-244-692833 Sequence 692833,

RESULT 1  
US-11-121-849-188861  
; Sequence 188861, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Formalin Fixed Paraffin Embedded  
; TITLE OF INVENTION: Microarray  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIORITY APPLICATION NUMBER: 60/567,949  
; PRIORITY FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1  
; SEQ ID NO: 188861  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-188861

Query Match 7.6%; Score 25; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
Qy 179 AGGCCTCCGTTACTTCAGAGACTG 203  
Db 1 AGGCCTCCGTTACTTCAGAGACTG 25

RESULT 2  
US-11-121-849-188862  
; Sequence 188862, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
; TITLE OF INVENTION: Microarray  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIORITY APPLICATION NUMBER: 60/567,949  
; PRIORITY FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1  
; SEQ ID NO: 188862  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-188862

```

; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 188862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188862

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188863
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188863

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2005-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188863
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188863

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188863
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188863

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2005-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188864
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188864

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2005-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188864
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188864

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188865
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188865

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2005-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188865
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188865

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188866
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188866

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2005-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188866
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188866

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188867
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188867

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Delins 0;
FILE REFERENCE: 3.684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIORITY FILING DATE: 2005-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 188867
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-188867

```



APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIOR APPLICATION NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIOR APPLICATION NUMBER: 60/426,137  
 PRIOR FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO: 692824  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-692824

RESULT 12  
 US-11-101-244-692826  
 Sequence 692826, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmacon, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIOR APPLICATION NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIOR APPLICATION NUMBER: 60/426,137  
 PRIOR FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO: 692826  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-692826

RESULT 13  
 US-11-101-244-692827  
 Sequence 692827, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmacon, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIOR APPLICATION NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIOR APPLICATION NUMBER: 60/426,137  
 PRIOR FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO: 692827  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-692827

Query Match 5.8%; Score 19; DB 10; Length 19;  
 Best Local Similarity 63.2%; Pred. No. 1.7;  
 Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 104 GGGATATCTGGTGTATAA 122  
 Db 1 GGGAUATGGUGGUAGAAA 19

Query Match 5.8%; Score 19; DB 10; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 1.7;  
 Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 291 CACAGAGACTGGGAACTC 309  
 Db 1 CACAGAGAGGGGAUUC 19

RESULT 14  
 US-11-101-244-692829  
 Sequence 692829, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmacon, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIOR APPLICATION NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIOR APPLICATION NUMBER: 60/426,137  
 PRIOR FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO: 692829  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-692829

Query Match 5.8%; Score 19; DB 10; Length 19;  
 Best Local Similarity 73.7%; Pred. No. 1.7;  
 Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 137 GGACCACTATTGATCT 155  
 Db 1 GGACCACTATTGATCT 19

RESULT 15  
 US-11-101-244-692830  
 Sequence 692830, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmacon, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA

```
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 692830
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692830

Query Match      5.8%: Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy          134 GCAGGAAACCACATTATGA 152
           |||||:|||||:||:||:|||:|
Db          1 GCAGGAAACCACAUUAGGA 19

Search completed: March 8, 2006, 14:44:48
Job time : 297.184 secs
```

This Page Blank (U.S.P. 1)

Post-processing: Listing first 45 summaries							
Maximum DB seq length: 0 Maximum DB seq length: 2000000000							
Database : Published Applications NA Main: *							
1: /cggn2_6_ptodata/1/pubbra/us07_pubcomb.seq*							
2: /cggn2_6_ptodata/1/pubbra/us08_pubcomb.seq*							
3: /cggn2_6_ptodata/1/pubbra/us09a_pubcomb.seq*							
4: /cggn2_6_ptodata/1/pubbra/us09b_pubcomb.seq*							
5: /cggn2_6_ptodata/1/pubbra/us10_pubcomb.seq*							
6: /cggn2_6_ptodata/1/pubbra/us10b_pubcomb.seq*							
7: /cggn2_6_ptodata/1/pubbra/us10c_pubcomb.seq*							
8: /cggn2_6_ptodata/1/pubbra/us10d_pubcomb.seq*							
9: /cggn2_6_ptodata/1/pubbra/us10e_pubcomb.seq*							
10: /cggn2_6_ptodata/1/pubbra/us11_pubcomb.seq*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
\$							
Result No.	Score	Query Match	Length	DB ID	Description		
1	327	100.0	433	7 US-10-242-535A-433177	Sequence 433177, A		
2	327	100.0	433	7 US-10-085-783A-433177	Sequence 433177, A		
3	327	100.0	453	7 US-10-242-535A-35025	Sequence 35025, A		
4	327	100.0	453	7 US-10-085-783A-35025	Sequence 35025, A		
5	327	100.0	467	7 US-10-242-535A-39933	Sequence 39933, A		
6	327	100.0	467	7 US-10-085-783A-39933	Sequence 39933, A		
7	327	100.0	471	7 US-10-242-535A-57254	Sequence 57254, A		
8	327	100.0	471	7 US-10-085-783A-57254	Sequence 57254, A		
9	327	100.0	472	7 US-10-242-535A-56068	Sequence 56068, A	Qy	1 ATGGGGCACCGATGATGGATAACCCAGCGGCCAACAGCGGCCATGGAAG 60
10	327	100.0	472	7 US-10-085-783A-56068	Sequence 56068, A	Db	20 ATGGGGCACCGATGATGGATAACCCAGCGGCCAACAGCGGCCATGGAAG 79
11	327	100.0	508	8 US-10-913-937-3	Sequence 3, App11		
12	327	100.0	523	7 US-10-242-535A-462292	Sequence 462292, A	Qy	61 CGCTTGAATGAAAGTCGAATCAGTAGGCCCTCTGGGCATTTGTGTTGAT 12
13	327	100.0	523	7 US-10-085-783A-462292	Sequence 462292, A	Db	80 CGCTTGAATGAAAGTCGAATCAGTAGGCCCTCTGGGCATTTGTGTTGAT 13
14	325	99.4	476	3 US-09-918-995-17191	Sequence 17191, A		
15	321	98.2	4543	5 US-10-198-846-11311	Sequence 11311, A		
16	308	94.2	4476	8 US-10-357-930-25604	Sequence 25604, A	Qy	121 AACGTGCCATCTGGGACCAATTGGATGTCAGTAACCTAACAG 18
17	296	90.5	3484	8 US-10-723-160-1383	Sequence 1383, AP	Db	140 AACGTGCCATCTGGGACCAATTGGATGTCAGTAACCTAACAG 19
18	295	90.5	3484	9 US-10-756-149-1357	Sequence 1357, AP		
19	295	90.5	5111	5 US-10-205-823-382	Sequence 382, App		
20	295	90.5	5111	10 US-11-051-454-382	Sequence 382, App		
21	295	90.5	5371	8 US-10-723-860-5852	Sequence 5852, AP	Qy	181 GCGTCCGCTACTTCAGAAGTGTACTGTGGCATGGCCCTCTGGGAGCTGTGTTTCAC 24
22	270	82.6	4668	7 US-10-242-535A-47656	Sequence 47656, A	Db	200 GCGTCCGCTACTTCAGAAGTGTACTGTGGCATGGCCCTCTGGGAGCTGTGTTTCAC 25
23	270	82.6	4668	7 US-10-085-783A-47656	Sequence 47656, A		



Best Local Similarity 100.0%; Pred. No. 1.8e-173; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 200 GCGTCGGCTACTTCAGAAGAGTGTACTGTGATGGGAGTCCTGTAACCATGCTTTCAAC 259  
 Qy 1 ATGGCCGCAAGGATGATGCCAGGGCAAGGGCAAGAAG 60  
 Db 24 ATGGCCGAGGGATGATGCCAGGGCAAGGGCAAGAAG 83  
 Qy 61 CGCTTGAGTGAAGTGAAGTGAATGCAATGGCTGGATAATTGGTTGAT 120  
 Db 84 CGCTTGAGTGAAGTGAAGTGAATGCAATGGCTGGATAATTGGTTGAT 143

RESULT 6  
 US-10-085-783A-39933  
 ; Sequence 39933, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTOR: Liwei, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIORITY APPLICATION NUMBER: US 60/305,340  
 ; PRIORITY FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIORITY FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIORITY FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 5894  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 39933  
 ; LENGTH: 467  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-085-783A-39933

Query Match 100.0%; Score 327; DB 7; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGGCGCGGAGATGGATACCCGAGCCAAAGGGCGGAGAAG 60  
 Db 20 ATGGGGCGCGGAGATGGATACCCGAGCCAAAGGGCGGAGAAG 79  
 Qy 61 CGTTGAGTGAAGTGAAGAAAGTGGTCAATTGGACAAAGAAG 120  
 Db 80 CGTTGAGTGAAGAAAGTGAATGCAATGGCCTCTGGCCCTGGGATATTGGTTGAT 139  
 Qy 121 AACGTGGCATCGATGATGCCAGGGACCAACAGCGGCAACAGGGCAAGAAG 180  
 Db 20 ATGGGGCGCGGAGATGGATACCCGAGCCAAAGGGCGGAGAAG 79  
 Qy 61 CGCTTGAGTGAAGTGAAGGGAATGGATATTGGCTGGATAAGTGTGTTGAT 120  
 Db 80 CGCTTGAGTGAAGGGAATGGATATTGGCTGGATAAGTGTGTTGAT 139  
 Qy 121 AACGTGGCATCGATGATGCCAGGGACCAACAGCGGCAACAGGGCAAGAAG 180  
 Db 140 AACGTGGCATCGATGATGCCAGGGACCAACAGCGGCAACAGGGCAAGAAG 199  
 Qy 121 AACGTGGCATCGATGATGCCAGGGACCAACAGCGGCAACAGGGCAAGAAG 240  
 Db 140 AACGTGGCATCGATGATGCCAGGGACCAACAGCGGCAACAGGGCAAGAAG 240  
 Qy 121 AACGTGGCATCGATGATGCCAGGGACCAACAGCGGCAACAGGGCAAGAAG 319  
 Db 140 AACGTGGCATCGATGATGCCAGGGACCAACAGCGGCAACAGGGCAAGAAG 319  
 Qy 121 AACGTGGCATCGATGATGCCAGGGACCAACAGCGGCAACAGGGCAAGAAG 346  
 Db 140 AACGTGGCATCGATGATGCCAGGGACCAACAGCGGCAACAGGGCAAGAAG 346

RESULT 7  
 US-10-242-535A-57254  
 ; Sequence 57254, Application US/10242535A  
 ; Publication No. US2004013663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTOR: Liwei, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

```

FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
SEQ ID NO 57254
LENGTH: 471
TYPE: DNA
ORGANISM: Human
US-10-242-535A-57254

Query Match Score 327; DB 7; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGGAGCGATGGATGGATACCCGAGGCCAACAGGGCGGCCAGAAAG 60
Db 17 ATGGCGGAGCGATGGATGGATACCCGAGGCCAACAGGGCGGCCAGAAAG 76
Qy 61 CGCTTGAAGTGAAGAAGTGGATACTGGAGCTGGATATTGGTTGAT 120
Db 77 CGCTTGAAGTGAAGAAGTGGATACTGGAGCTGGATATTGGTTGAT 136
Qy 1 ATGGCGGAGCGATGGATGGATACCCGAGGCCAACAGGGCGGCCAGAAAG 60
Db 17 ATGGCGGAGCGATGGATGGATACCCGAGGCCAACAGGGCGGCCAGAAAG 76
Qy 61 CGCTTGAAGTGAAGAAGTGGATACTGGAGCTGGATATTGGTTGAT 120
Db 77 CGCTTGAAGTGAAGAAGTGGATACTGGAGCTGGATATTGGTTGAT 136
RESULT 9
US-10-242-535A-56068
; Sequence 56068, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patentin version 3.2
SEQ ID NO 56068
LENGTH: 472
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (437)..(437)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (455)..(455)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-56068

Query Match Score 327; DB 7; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGGAGCGATGGATGGATACCCGAGGCCAACAGGGCGGCCAGAAAG 60
Db 20 ATGGCGGAGCGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 120
Qy 61 CGCTTGAAGTGAAGAAGTGGATACTGGAGCTGGATATTGGTTGAT 120

```



Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY OR AGENT: Liew, C. C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIORITY NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIORITY NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIORITY NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIORITY NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 46292  
; LENGTH: 523  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-242-535A-46292

---

Query Match 100.0%; Score 327; DB 7; Length 523;  
Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCGCAGGATGGATGCTGGATAACCCGAGGGACCAACAGGGGGCAAAAGGAG 60  
Db 19 ATGGCGCAGGATGGATGCTGGATAACCCGAGGGACCAACAGGGGGCAAAAGGAG 78  
QY 61 CGTTTGAAAGTGAaaaaAGTGGATGGATGGCTGGGATGGATGGCTGGATGGTGTGAT 120  
Db 79 CGTTTGAAAGTGAaaaaAGTGGATGGATGGCTGGGATGGATGGCTGGATGGTGTGAT 138  
QY 121 AACTGTGCCATCTCGAGAAACCAATTGGATGGCTGGGATGGCTGGATGGCTGG 300  
Db 199 GCGTCGGTACTTGGATGGCTGGGATGGCTGGGATGGCTGGATGGCTGG 318  
QY 241 TTCACTGCATCTCGCTGGCTGGCTGGCTGGGACTAG 327  
Db 259 TTCACTGCATCTCGCTGGCTGGCTGGGACTAG 345  
RESULT 14  
Sequence 17191, Application US/09918995  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; PUBLICATION NO. US20030073623A1  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FROM VARIOUS cDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,395  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq For Windows Version 3.0  
SEQ ID NO 17191  
; LENGTH: 476  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1) .. (476)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-17191

---

Query Match 99.4%; Score 325; DB 3; Length 476;  
Best Local Similarity 100.0%; Pred. No. 2.4e-172;  
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGCGCAGGATGGATGGCTGGATAACCCGAGGGACCAACAGGGGGCAAAAGGCG 62  
Db 74 GGCGCAGGATGGATGGCTGGATAACCCGAGGGACCAACAGGGGGCAAAAGGCG 133  
QY 63 CTTGAAGTAAAGTGGATGGCTGGGCTGGATGGTGTGATAA 122  
Db 134 CTTGAAGTAAAGTGGATGGCTGGGCTGGATGGTGTGATAA 193  
QY 123 CTGTCGCCATCTGGAGAACCAATTGGATCTGGCATGAAATGTCAGGTCACAGGC 182  
SEQ ID NO 46292

RESULT 15  
 US-10-198-846-11311/c  
 ; Sequence 11311, Application US/10198846  
 ; Publication No. US2003009974A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Xu, Yongyao  
 ; APPLICANT: Wang, Youzhen  
 ; STEINMANN, Kathleen  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 ; FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; TREATMENT OF BREAST CANCER  
 ; FILE REFERENCE: MRI-049  
 ; CURRENT APPLICATION NUMBER: US/10/198, 846  
 ; CURRENT FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/306, 220  
 ; PRIOR FILING DATE: 2001-07-18  
 ; NUMBER OF SEQ ID NOS: 14084  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 11311  
 ; LENGTH: 4543  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-198-846-11311

Query Match 98.2%; Score 321; DB 5; Length 4543;  
 Best Local Similarity 100.0%; Pred. No. 4\_3e-170;  
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCAGCGATGGATGTGGATACCCAGGCCACCAACGGCGGGAAAGGGCTTT 66  
 DB 1085 GCACCGATGGATGTGGATACCCAGGCCACCAACGGCGGGAAAGGGCTTT 1026  
 QY 67 GAAGTGAAAAAGTGGAAATGCACTGGCCTCTGGGCTGGATAATTGGCTTGATAAACGT 126  
 DB 1025 GAAGTGAAAAAGTGGAAATGCACTGGCCTCTGGGCTGGGATATTGGCTTGATAAACGT 966  
 QY 127 GCCATCTGAGGAAACCATATTGGATCTTGCATAGATGTCAGCTAACGGCGTCC 186  
 DB 965 GGCATCTGAGGAAACCATATTGGATCTTGCATAGATGTCAGCTAACGGCGTCC 906  
 QY 187 GCTACTTCAAGAAGTGTACTGGCATGGGAGTCGTAAACCATTGGTTTCACTTCAC 246  
 DB 905 GCTACTTCAAGAAGTGTACTGGCATGGGAGTCGTAAACCATTGGTTTCACTTCAC 846  
 QY 247 TGCATCTCTGGCTGCTCAAACACGAAAGGTGTCAATTGGACAACAGAAGTGGGAA 306  
 DB 845 TGCATCTCTGGCTGCTCAAACACGAAAGGTGTCAATTGGACAACAGAAGTGGGAA 786  
 QY 307 TTCCAAAAGTATGGGCACTAG 327  
 DB 785 TTCCAAAAGTATGGGCACTAG 765

This Page Blank (USPS)

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using SW model.

Run on: March 8, 2006, 13:03:41 ; Search time 112.91 Seconds  
 (without alignments)  
 5148.003 Million cell updates/sec

Title: US-09-541-462B-1  
 Perfect score: 327  
 Sequence: 1 atgcgcggatggatgt.....tccaaaatggcactag 3.27

Scoring table: OLIGO\_NUC  
 Gapext 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 12

Total number of hits satisfying chosen parameters: 26735

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :	Issued Patents NA:*
1:	/cgcn2_6/ptodata/1/ina/1_COMB.seq:*
2:	/cgcn2_6/ptodata/1/ina/5_COMB.seq:*
3:	/cgcn2_6/ptodata/1/ina/6A_COMB.seq:*
4:	/cgcn2_6/ptodata/1/ina/6B_COMB.seq:*
5:	/cgcn2_6/ptodata/1/ina/H_COMB.seq:*
6:	/cgcn2_6/ptodata/1/ina/POTUS_COMB.seq:*
7:	/cgcn2_6/ptodata/1/ina/PP_COMB.seq:*
8:	/cgcn2_6/ptodata/1/ina/R_COMB.seq:*
9:	/cgcn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	482	3	US-09-513-999C-3894
2	327	100.0	507	3	US-09-949-016-1940
3	327	100.0	508	3	US-09-914-324A-3
4	249	76.1	3208	3	US-09-780-16-27
5	249	76.1	3208	3	US-10-214-811-27
6	249	76.1	3208	3	US-10-766-074-27
7	170	52.0	402	3	US-09-599C-1031
8	170	52.0	463	3	US-09-621-976-15180
9	89	27.2	25274	3	US-09-949-016-16682
10	50	15.3	504	3	US-09-914-324A-5
11	36	11.0	601	3	US-09-949-016-174803
12	20	6.1	411	3	US-09-640-211A-1731
c 13	18	5.5	902	3	US-09-270-767-16361
c 14	18	5.5	3183	2	US-08-939-218A-1
c 15	18	5.5	3183	2	PCT-US95-06815-1
c 16	18	5.5	3187	6	US-08-666-037-26
c 17	18	5.5	3192	2	US-08-940-661A-1
c 18	18	5.5	3192	2	US-09-083-485-1
c 19	18	5.5	3192	2	US-09-005-397-26
c 20	18	5.5	3192	2	US-08-119-125A-3
c 21	18	5.5	4118	2	US-09-5653
c 22	18	5.5	63563	3	US-09-5949-016-16976
c 23	18	5.5	113283	3	US-09-949-016-16977
c 24	18	5.5	113283	3	Sequence 16977, A

Sequence 12537, A  
 Sequence 2439, AP  
 Sequence 79297, A  
 Sequence 174631,  
 Sequence 14, Appl  
 Sequence 4, Appl  
 Sequence 13, Appl  
 Sequence 76, Appl  
 Sequence 86, Appl  
 Sequence 16395, A  
 Sequence 597, APP  
 Sequence 1533, AP  
 Sequence 99, Appl  
 Sequence 15271, A  
 Sequence 15272, A  
 Sequence 13399, A  
 Sequence 12339, A  
 Sequence 13275, A  
 Sequence 16678, A  
 Sequence 64, Appl  
 Sequence 14033, A

ALIGNMENTS

RESULT 1  
 US-09-513-999C-3894  
 sequence 3894, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumais Milne Edwards, J.B.  
 ; ATTORNEY: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; Patent No. 6783961  
 ; FILE REFERENCE: 5.9.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; CURRENT FILING DATE: 2000-02-24  
 ; PRIORITY APPLICATION NUMBER: US 1999-02-26  
 ; PRIOR FILING DATE: 1999-02-26  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.pmm  
 ; SEQ ID NO: 3894  
 ; LENGTH: 482  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 29..352  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 401  
 ; OTHER INFORMATION: r=a or g  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 404  
 ; OTHER INFORMATION: m=a or c  
 ; US-09-513-999C-3894

Query Match 100.0%; Score 327; DB 3; Length 482;  
 Best local Similarity 100.0%; Prd. No. 7.3e-167;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGCGATGGATGTGGATACCCGAGCGCACCAACCGGGGAGAAG 60  
 Db 29 ATGGCGGAGCGATGGATGTGGATACCCGAGCGCACCAACCGGGGAGAAG 88  
 Qy 61 CGCTTGAATGAACTGGAAATGCAATGGCTGGATATTGGTTGTAT 120  
 Db 89 CGCTTGAATGAACTGGAAATGCAATGGCTGGATATTGGTTGTAT 148  
 Qy 121 AACGTGTGCCATCTGGAAACCAATTGGATCTTGATGAACTAACCTAAC 180

RESULT 2  
 US-09-949-016-4940  
 ; Sequence 4940, Application US/09949016  
 ; Patent No. 6812339

GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CLO01307  
 CURRENT APPLICATION NUMBER: US/097949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 4940  
 LENGTH: 507  
 TYPE: DNA  
 ORGANISM: Human  
 US-09-949-016-4940

Query Match 100.0%; Score 327; DB 3; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-167;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ATGGCGCACCGATGTTGAGTACCCCGAGGCCAACGAGGCTGGATCTGGCCTCTGGGCCTGGGATATTGGCTGTGAT 120  
 Db 67 CGCTTGAACTGAAAAGTGGTAATGGCTGGGCTGGATATTGGCTGTGAT 120  
 Db 121 AACGTGCCATTGGGACCAATTGGATGATGATGCTGGATGGCTGGGACT 180  
 Db 127 AACGTGCCATTGGGACCAATTGGATGATGCTGGATGGCTGGGACT 180  
 Db 181 GCGTCGGTACTTCAGAAGGTGACTGTGCACTGGGAGTCGTGATGGCTGGGACT 186  
 Db 187 GCGTCGGTACTTCAGAAGGTGACTGTGCACTGGGAGTCGTGATGGCTGGGACT 186  
 Db 241 TTCCACTGCATCTCGCTGGCTAAACAGCACGGTGTGTCATTGGACAACAGAGAG 300  
 Db 247 TTCCACTGCATCTCGCTGGCTAAACAGCACGGTGTGTCATTGGACAACAGAGAG 306  
 Qy 61 CGCTTGAACTGAAAAGTGGTAATGGCTGGGCTGGATATTGGCTGTGAT 120  
 Qy 67 CGCTTGAACTGAAAAGTGGTAATGGCTGGGCTGGATATTGGCTGTGAT 126  
 Db 121 AACGTGCCATTGGGACCAATTGGATGATGCTGGATGGCTGGGACT 180  
 Db 127 AACGTGCCATTGGGACCAATTGGATGATGCTGGATGGCTGGGACT 186  
 RESULT 4  
 US-09-780-016-27  
 ; Sequence 27, Application US/09780016  
 ; Patent No. 6509456  
 GENERAL INFORMATION:  
 APPLICANT: Donoho, Gregory  
 APPLICANT: Scoville, John  
 APPLICANT: Turner, C. Alexander Jr.  
 APPLICANT: Friedrich, Glenn  
 APPLICANT: Abuin, Alejandro  
 APPLICANT: Zambrowicz, Brian  
 APPLICANT: Saada, Arthur T.  
 TITLE OF INVENTION: No. 6509456 Human Proteases and Polynucleotides Encoding the Same  
 TITLE OF INVENTION: LEX-0132-USA  
 FILE REFERENCE: US/09-914-324A-3  
 CURRENT APPLICATION NUMBER: US/09/780,016  
 CURRENT FILING DATE: 2001-02-09

RESULT 3  
 US-09-914-324A-3  
 ; Sequence 3, Application US/09914324A

PRIOR APPLICATION NUMBER: US 60/181,294  
 PRIOR FILING DATE: 2000-02-11  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 27  
 LENGTH: 3208  
 TYPE: DNA  
 ORGANISM: homo sapiens  
 US-09-780-016-27

Query Match 76.1%; Score 249; DB 3; Length 3208;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-124;  
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 TGGATGCACTAGCCCTCTGGGCCCTGGATATTGGTGTGATAACTGTGCCATCTGCAGG 138  
 Db 2776 TGGATGCACTAGCCCTCTGGGCCCTGGATATTGGTGTGATAACTGTGCCATCTGCAGG 2835

RESULT 6  
 US-10-766-074-27  
 ; Sequence 27, Application US/10766074  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donoho, Gregory  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Abuin, Alejandro  
 ; APPLICANT: Zambrowicz, Brian  
 ; APPLICANT: Sands, Arthur T.  
 ; TITLE OF INVENTION: Polynucleotides Encoding the Same  
 ; FILE REFERENCE: LEX-0132-USA  
 ; CURRENT FILING DATE: 2004-01-28  
 ; PRIORITY APPLICATION NUMBER: US/10/766,074  
 ; PRIORITY FILING DATE: 2002-08-07  
 ; PRIORITY APPLICATION NUMBER: US/09/780,016  
 ; SEQ ID NO: 27  
 ; PRIORITY FILING DATE: 2001-02-09  
 ; PRIORITY APPLICATION NUMBER: US 60/181,294  
 ; LENGTH: 3208  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-10-766-074-27

Query Match 76.1%; Score 249; DB 3; Length 3208;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-124;  
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 GAGTGTACTGTCGATGGGAGTTGTTACATGCTTCAGTCTCGC 258  
 Db 2896 GAGTGTACTGTCGATGGGAGTTGTTACATGCTTCAGTCTCGC 2955

Qy 139 AACCATATTGGATCTTGATAGAACTGGTCAAGTAACAGGCTCCGTTACTTCAGAA 198  
 Db 2836 AACCATATTGGATCTTGATAGAACTGGTCAAGTAACAGGCTCCGTTACTTCAGAA 2895

Qy 199 GAGTGTACTGTCGATGGGAGTTGTTACATGCTTCAGTCTCGC 258  
 Db 2896 GAGTGTACTGTCGATGGGAGTTGTTACATGCTTCAGTCTCGC 2955

Qy 259 TGGCTCAAAACAGCACAGGTGTGTCATGGACACACAGAGTGGAAATTCCAAAAGPAT 318  
 Db 2956 TGGCTCAAAACAGCACAGGTGTGTCATGGACACACAGAGTGGAAATTCCAAAAGPAT 3015

Qy 319 GGGCACTAG 327  
 Db 3016 GGGCACTAG 3024

RESULT 5  
 US-10-214-811-27  
 ; Sequence 27, Application US/10214811  
 ; Patent No. 6743621  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donoho, Gregory  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Abuin, Alejandro  
 ; APPLICANT: Zambrowicz, Brian  
 ; TITLE OF INVENTION: No. 6743621el Human Proteases and  
 ; FILE REFERENCE: LEX-0132-USA  
 ; CURRENT FILING DATE: 2002-08-07  
 ; PRIORITY APPLICATION NUMBER: US/09/780,016  
 ; PRIORITY FILING DATE: 2001-02-09  
 ; PRIORITY APPLICATION NUMBER: US 60/181,294  
 ; NUMBER OF SEQ ID NOS: 27  
 ; LENGTH: 3208  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 27  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-10-214-811-27

Query Match 76.1%; Score 249; DB 3; Length 3208;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-124;  
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 TGGATGCACTAGCCCTCTGGGCCCTGGATATTGGTGTGATAACTGTGCCATCTGCAGG 138  
 Db 2776 TGGATGCACTAGCCCTCTGGGCCCTGGATATTGGTGTGATAACTGTGCCATCTGCAGG 2835

Qy 139 AACCATATTGGATCTTGATGGGAGTTGTTACATGCTTCAGTCTCGC 198  
 Db 2836 AACCATATTGGATCTTGATGGGAGTTGTTACATGCTTCAGTCTCGC 2895

Qy 199 GAGTGTACTGTCGATGGGAGTTGTTACATGCTTCAGTCTCGC 258  
 Db 2896 GAGTGTACTGTCGATGGGAGTTGTTACATGCTTCAGTCTCGC 2955

Qy 259 TGGCTCAAAACAGCACAGGTGTGTCATGGACACACAGAGTGGAAATTCCAAAAGPAT 318  
 Db 2956 TGGCTCAAAACAGCACAGGTGTGTCATGGACACACAGAGTGGAAATTCCAAAAGPAT 3015

Qy 319 GGGCACTAG 327  
 Db 3016 GGGCACTAG 3024

RESULT 7

US-09-513-999C-10371  
*; Sequence 10371, Application US/09513999C*  
*; Patent No. 6783961*  
*; GENERAL INFORMATION:*  
*; APPLICANT: Dumas Milne Edwards, J.B.*  
*; APPLICANT: Duclerc, A.*  
*; APPLICANT: Giordano, J.Y.*  
*; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.*  
*; Patent No. 6783961*  
*; FILE REFERENCE: 59 US2. REG*  
*; CURRENT APPLICATION NUMBER: US/09/513, 999C*  
*; CURRENT FILING DATE: 2000-02-24*  
*; PRIOR APPLICATION NUMBER: US 60/122, 487*  
*; PRIOR FILING DATE: 1999-02-26*  
*; NUMBER OF SEQ ID NOS: 36681*  
*; SOFTWARE: Patent .pm*  
*; SEQ ID NO: 10371*  
*; LENGTH: 402*  
*; TYPE: DNA*  
*; ORGANISM: Homo sapiens*  
*; FEATURE: misc\_feature*  
*; LOCATION: 20*  
*; OTHER INFORMATION: k=g or t*  
*; FEATURE: misc\_feature*  
*; NAME/KEY: misc\_feature*  
*; LOCATION: 38*  
*; OTHER INFORMATION: s=g or c*  
*; FEATURE: misc\_feature*  
*; LOCATION: 79*  
*; OTHER INFORMATION: n=a, g, c or t*  
*; US-09-513-999C-10371*

Query Match 52.0%; Score 170; DB 3; Length 402;  
Best Local Similarity 100.0%; Pred. No. 6.0e-82;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGAATGCAAGCTAACCGGTCTGGTCAAGTGTAATTCAAGGTCATGG 217  
Db 106 GCATAGAATGCAAGCTAACCGGTCTGGTCAAGTGTAATTCAAGGTCATGG 165  
Qy 218 GAGTCTGTAACCATGCTTTACTTCACAGTCATGCTCGCTCAAAACAGACAG 277  
Db 166 GAGTCTGTAACCATGCTTTACTTCACAGTCATGCTCGCTCAAAACAGACAG 225  
Qy 278 TGTCGCCATTGGACAAACAGAGTGCGGAATTCCAAAATGATGGCACTAG 327  
Db 226 TGTCGCCATTGGACAAACAGAGTGCGGAATTCCAAAATGATGGCACTAG 275

RESULT 8  
US-09-621-976-15180  
*; Sequence 15180, Application US/09621976*  
*; Patent No. 6639063*  
*; GENERAL INFORMATION:*  
*; APPLICANT: Dumas Milne Edwards, J.B.*  
*; APPLICANT: Giordano, J.Y.*  
*; TITLE OF INVENTION: ESTs and Encoded Human Proteins.*  
*; FILE REFERENCE: GENSET.054PR2*  
*; CURRENT APPLICATION NUMBER: US/09/621, 976*  
*; CURRENT FILING DATE: 2000-07-21*  
*; NUMBER OF SEQ ID NOS: 19335*  
*; SOFTWARE: Patent .pm*  
*; SEQ ID NO: 15180*  
*; LENGTH: 463*  
*; TYPE: DNA*  
*; ORGANISM: Homo sapiens*  
*; FEATURE: misc\_feature*  
*; LOCATION: 74*  
*; OTHER INFORMATION: n=a, g, c or t*

US-09-621-976-15180  
Query Match 52.0%; Score 170; DB 3; Length 463;  
Best Local Similarity 100.0%; Pred. No. 6.9e-82;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGAATGCAAGCTAACCGGTCTGGTCAAGTGTAATTCAAGGTCATGG 217  
Db 101 GCATAGAATGCAAGCTAACCGGTCTGGTCAAGTGTAATTCAAGGTCATGG 165  
Qy 218 GAGTCTGTAACCATGCTTTACTTCACAGTCATGCTCGCTCAAAACAGACAG 277  
Db 161 GAGTCTGTAACCATGCTTTACTTCACAGTCATGCTCGCTCAAAACAGACAG 220  
Qy 278 TGTCGCCATTGGACAAACAGAGTGCGGAATTCCAAAATGATGGCACTAG 327  
Db 221 TGTCGCCATTGGACAAACAGAGTGCGGAATTCCAAAATGATGGCACTAG 270

RESULT 9  
US-09-949-016-16682  
*; Sequence 16682, Application US/09949016*  
*; Patent No. 6812339*  
*; GENERAL INFORMATION:*  
*; APPLICANT: VENTER, J. Craig et al.*  
*; TITLE OF INVENTION: KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF*  
*; FILE REFERENCE: CLO01307*  
*; CURRENT APPLICATION NUMBER: US/09/949, 016*  
*; CURRENT FILING DATE: 2000-04-14*  
*; PRIORITY APPLICATION NUMBER: 60/241, 755*  
*; PRIORITY FILING DATE: 2000-10-20*  
*; PRIORITY APPLICATION NUMBER: 60/237, 768*  
*; PRIORITY FILING DATE: 2000-10-03*  
*; PRIORITY APPLICATION NUMBER: 60/231, 498*  
*; PRIORITY FILING DATE: 2000-09-08*  
*; NUMBER OF SEQ ID NOS: 20012*  
*; SOFTWARE: FastSEQ for Windows Version 4.0*  
*; SEQ ID NO: 16682*  
*; LENGTH: 25274*  
*; TYPE: DNA*  
*; ORGANISM: Human*  
*; US-09-949-016-16682*

Query Match 27.2%; Score 89; DB 3; Length 25274;  
Best Local Similarity 100.0%; Pred. No. 5.4e-38;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 CATGTTTTCACCTTCACAGTCATGCTCGCTCAAAACACAGACAGTCATGG 288  
Db 18411 CNTGTTTTCACCTTCACAGTCATGCTCGCTCAAAACACAGACAGTCATGG 18470

RESULT 10  
US-09-949-324A-5  
*; Sequence 5, Application US/09914324A*  
*; Patent No. 6858709*  
*; GENERAL INFORMATION:*  
*; APPLICANT: Conway, Joan A.*  
*; APPLICANT: Conway, Ronald C.*  
*; APPLICANT: Kamura, Takumi*  
*; APPLICANT: Okamoto Medical Research Foundation*  
*; TITLE OF INVENTION: von Hippel-Lindau Tumor Suppressor Complex and SCP Ubiquitin Ligase*  
*; FILE REFERENCE: 021044-0146001JS*  
*; CURRENT APPLICATION NUMBER: US/09/914, 324A*  
*; CURRENT FILING DATE: 2003-02-11*  
*; PRIORITY APPLICATION NUMBER: US 60/121, 787*  
*; PRIORITY FILING DATE: 1999-02-26*

```

; PRIOR APPLICATION NUMBER: WO_PCT/US00/04838
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-09-914-324A-5

Query Match          15.3%;  Score 50;  DB 3;  Length 504;
Best Local Similarity 100.0%;  Pred. No. 6.1e-17;
Matches 50;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    109 ATTGCGTTGATAACTGTGCCATCNGCAGAACCATATGGATCTTG 158
Db    126 ATTGCGTTGATAACTGTGCCATCNGCAGAACCATATGGATCTTG 175
                                         RESULT 13
                                         US-09-270-767-26361/C
                                         Sequence 26361, Application US/09270767
                                         ; GENERAL INFORMATION:
                                         ; Patent No. 6703491
                                         ; APPLICANT: Homberger et al.
                                         ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                         ; FILE REFERENCE: File Reference: 7326-094
                                         ; CURRENT APPLICATION NUMBER: US/09/270,767
                                         ; CURRENT FILING DATE: 1999-03-17
                                         ; NUMBER OF SEQ ID NOS: 62517
                                         ; SOFTWARE: PatentIn Ver. 2.0
                                         ; SEQ ID NO: 26361
                                         ; LENGTH: 287
                                         ; TYPE: DNA
                                         ; ORGANISM: Drosophila melanogaster
                                         ; FEATURE:
                                         ; OTHER INFORMATION: n means any nucleotide
                                         US-09-270-767-26361

                                         Query Match          5.5%;  Score 18;  DB 3;  Length 287;
                                         Best Local Similarity 100.0%;  Pred. No. 12.3e-01;
                                         Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    299 AGTGGAAATTCCAAGT 316
Db    113 AGTGGAAATTCCAAGT 96
                                         RESULT 14
                                         US-09-270-767-10881/C
                                         Sequence 10881, Application US/09270767
                                         ; GENERAL INFORMATION:
                                         ; Patent No. 6703491
                                         ; APPLICANT: Homberger et al.
                                         ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                         ; FILE REFERENCE: File Reference: 7326-094
                                         ; CURRENT APPLICATION NUMBER: US/09/270,767
                                         ; CURRENT FILING DATE: 1999-03-17
                                         ; NUMBER OF SEQ ID NOS: 62517
                                         ; SOFTWARE: PatentIn Ver. 2.0
                                         ; SEQ ID NO: 10881
                                         ; LENGTH: 902
                                         ; TYPE: DNA
                                         ; ORGANISM: Drosophila melanogaster
                                         ; FEATURE:
                                         ; OTHER INFORMATION: n means any nucleotide
                                         US-09-270-767-10881

                                         Query Match          5.5%;  Score 18;  DB 3;  Length 902;
                                         Best Local Similarity 100.0%;  Pred. No. 13.0e-01;
                                         Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    299 AGTGGAAATTCCAAGT 316

```

Db 728 AGTGGAAATTCCAAAAGT 711

---

RESULT 15  
US-08-939-218A-1/c  
Sequence 1, Application US/08939218A  
Patent No. 5981243

GENERAL INFORMATION:

APPLICANT: BERKA, Randy Michael  
APPLICANT: BROWN, Stephen H.  
APPLICANT: XU, Feng  
APPLICANT: SCHNEIDER, Palle  
APPLICANT: OXENBLL, Karen M.  
APPLICANT: AASLYNG, Dorrit A.  
TITLE OF INVENTION: PURIFIED MYCETOLOPHTHORA LACCASES AND NUCLEIC ACIDS ENCODING SAME

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5981243o No. 5981243disk of No. 5981243th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,218A  
FILING DATE: 29-SEPT-1997  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Rozek, Carol E.  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 4184.120-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-667-0123  
TELEFAX: 212-879-9655

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3183 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS  
LOCATION: join(586..831, 917..994, 1079..1090, 1193..1264,  
LOCATION: 1337..2308, 2456..2524, 2618..3028)  
US-08-939-218A-1

Query Match 5.5%; Score 18; DB 2; Length 3183;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 198 AGAGTCACTGTCGATG 215  
Db 924 AGAGTCACTGTCGATG 907

Search completed: March 8, 2006, 14:34:35  
Job time : 114.91 secs

Copyright GenCore version 5.1.7  
(c) 1993 - 2006 Biocceleration Ltd.

CM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 10:15:10 ; Search time 3736 Seconds  
(without alignments)  
4095.122 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1 atccggcaggatggatgt.....tccaaaatggcactag 327

Scoring table: OLIGO\_NUC

Gapext\_60.0 Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 12

Total number of hits satisfying chosen parameters: 897482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Listing first 45 summaries

Database : EST\*

- 1: 9b\_est1:\*
- 2: 9b\_est2:\*
- 3: 9b\_est3:\*
- 4: 9b\_hrc:\*
- 5: 9b\_est4:\*
- 6: 9b\_est5:\*
- 7: 9b\_est6:\*
- 8: 9b\_est7:\*
- 9: 9b\_gsa1:\*
- 10: 9b\_gss2:\*
- 11: 9b\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	462	CN305890	CN305890 170005830
2	327	100.0	471	BG339057	BG339057 60436882
3	327	100.0	473	BX283972	BX283972 BX283972
4	327	100.0	488	BG777485	BG777485 602664820
5	327	100.0	498	CB295618	CB295618 12B22006
6	327	100.0	509	CN305892	CN305892 170005831
7	327	100.0	518	BP420485	BP420485 BP420485
8	327	100.0	522	AL711573	AL711573 DKFZp686I
9	327	100.0	525	BG337472	BG337472 602435003
10	327	100.0	527	BM715215	BM715215 UI-E-CL1-
11	327	100.0	527	BH32751	BH32751 AGENCOURT
12	327	100.0	527	CB999822	CB999822 AGENCOURT
13	327	100.0	529	BMT57406	BMT57406 K-EST036
14	327	100.0	521	CD523457	CD523457 AGENCOURT
c 15	327	100.0	533	BUT29963	BUT29963 UI-E-CK1-
16	327	100.0	537	BC4786522	BC4786522 60255509
17	327	100.0	504	B0941262	B0941262 AGENCOURT
18	327	100.0	546	BT198015	BT198015 602767132
19	327	100.0	546	BU601181	BU601181 AGENCOURT
20	327	100.0	548	AV16338	AV16338 AV16338
21	327	100.0	548	BU601301	BU601301 AGENCOURT
22	327	100.0	549	BI858425	BI858425 603386437

## ALIGNMENTS

RESULT 1  
CN305890  
LOCUS CN305890  
DEFINITION 17000583044616 GRN\_PRBHEP Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN305890  
VERSION CN305890.1 GI:41722304  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Butheria; Euarchontoglires; Primates; Catahrini;  
Homidae; Homo  
1 (bases 1 to 462)

REFERENCE  
AUTHORS Brandenberger,R., Wei,R., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J. and Stanton,L.W.  
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation  
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)  
PUBMED 15146197  
COMMENT Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8656  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 412 Std Error: 0.00  
Location/Qualifiers  
FEATURES Source  
1 . 462  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, DMSO-treated H9 cell line"  
/clone\_lib="GRN\_PRBHEP"  
/note="Tolgo dt primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

ORIGIN  
Query Match 100.0%; Score 327; DB 7; Length 462;  
Best Local Similarity 100.0%; Pred. No. 6.6e-175;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCGAGGGATGGATGTGGATACCCGAGCGGCCAACAGGGCGGGCAAGAAG 60  
 Db 23 ATGGCCGAGGGATGGATGTGGATACCCAGCGCAGAACAGGGCGGGCAAGAAG 82

Qy 61 CGCTTGAAGTAAAGGTGAAATGCGATGCCCTCTGGATGGATAATTGGCTGAT 120  
 Db 83 CGCTTGAAGTAAAGGTGAAATGCGATGGATGCCCTCTGGCTGGATAATTGGCTGAT 142

Qy 121 AACTGTCGCCATCTGAGGAGCCATTAATGATCTTGATAGATGTAACTAAC 180  
 Db 143 AACTGTCGCCATCTGAGGAGCCATTAATGATCTGAACTAAC 202

Qy 181 CGGTCCGGCTACTTCAGAGGTGTAATGGGAGCTGTAAACATGTTTCAC 240  
 Db 203 CGTCCGGCTACTTCAGAGGTGTAATGGGAGCTGTAAACATGTTTCAC 262

Qy 241 TTCCACTGCATCTCGCTGCTCAAACACGACAGGTGTCATGGACTCTGTAACC 300  
 Db 263 TTCCACTGCATCTCGCTGCTCAAACACGACAGGTGTCATGGCAACAGAG 322

Qy 301 TGGGAATTCAAAAGTAGTGGCACTAG 327  
 Db 323 TGGGAATTCAAAAGTAGTGGCACTAG 349

Qy 301 TGGGAATTCAAAAGTAGTGGCACTAG 327  
 Db 342 TGGGAATTCAAAAGTAGTGGCACTAG 368

---

**RESULT 2**  
 BG339057 LOCUS BG339057 471 bp mRNA linear EST 27-FEB-2001  
 DEFINITION 602436882 F1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4554597 5',  
 mRNA sequence.

ACCESSION BG339057  
 VERSION 1  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominoidea; Homo.

REFERENCE 1 (bases 1 to 471)  
 AUTHORS NIH-MGC  
 TITLE NIH-MGC http://mgc.ncbi.nih.gov/  
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
 COMMENT Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgsaps-r@mail.nih.gov  
 Tissue Procurement: NIGC  
 DNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:  
<http://image.liln.gov>  
 Plate: LILCM154 row: d column: 22  
 High quality sequence stop: 470.

**FEATURES**  
 source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref=taxon:9606"  
 /clone="IMAGE:4554597"  
 /tissue\_type="leionyosarcoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH\_MGC\_46"  
 /note="Organ: uterus; Vector: pOB7; Site\_1: XbaI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

**ORIGIN**

Query Match Score 327; DB 2; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 6.e-175;  
 Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCGAGGGATGGATGTGGATACCCGAGCGGCCAACAGGGCGGGCAAGAAG 60  
 Db 42 ATGGCCGAGGGATGGATGTGGATACCCGAGGCCAACAGGGCGGGCAAGAAG 101

Qy 61 CGCTTGAAGTAAAGGTGAAATGCGATGCCCTCTGGATGGATAATTGGCTGAT 120  
 Db 102 CGCTTGAAGTAAAGGTGAAATGCGATGGATGCCCTCTGGCTGGATAATTGGCTGAT 161

Qy 121 AACGTGCCATCTCGAGGAGCCATTAATGATCTTGATAGATGTAACTAAC 180  
 Db 121 AACGTGCCATCTCGAGGAGCCATTAATGATCTTGATAGATGTAACTAAC 180

Qy 162 AACGTGCCATCTCGAGGAGCCATTAATGATCTTGATAGATGTAACTAAC 221

Db 181 GCGTCGGTACTTCAGAAGGTGTAATGGGAGCTGTGCTAACATGTTTCAC 240  
 Db 222 GCGTCGGTACTTCAGAAGGTGTAATGGGAGCTGTGCTAACATGTTTCAC 281

Qy 241 TTCCACTGCATCTCGCTGCTCAAACACGACAGGTGTCATGGACTCTGTAACC 300  
 Db 282 TTCCACTGCATCTCGCTGCTCAAACACGACAGGTGTCATGGACTCTGTAACC 349

Qy 301 TGGGAATTCAAAAGTAGTGGCACTAG 327  
 Db 342 TGGGAATTCAAAAGTAGTGGCACTAG 368

**RESULT 3**  
 BX283972 LOCUS BX283972 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:958P131435 ;  
 DEFINITION BX283972 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:4652028, mRNA sequence.

ACCESSION BX283972  
 VERSION BX283972.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 473)  
 AUTHORS Ebert L., Heil O., Hennig S., Neubert P., Partsch E., Peters M., Radeloff U., Schneider D. and Korn B.  
 TITLE Human UniGeneSet - RZPD3  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany  
 tel: +49 30 32639 101  
 fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libno=972)  
 This clone is available royalty-free from RZPD, contact RZPD (clone@rzpd.de) for further information. Seq primer: pCMV-M13u, Primer sequence: CGTTGTAAGAACGAGGCCAGT. Location/Qualifiers  
 1..473  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref=taxon:9606"  
 /clone="IMAGE:4554597"  
 /tissue\_type="leionyosarcoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: uterus; Vector: pOB7; Site\_1: XbaI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
 /clone\_id="NIH\_MGC\_21"  
 /note="Organ: placenta; Vector: pOTB7; Site\_1: XhoI;"

Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCACGGAG(G). Site-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 473;  
Best Local Similarity 100.0%; Pred. No. 6.6e-175;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCCcAGGGATGGATGTTGATAACCCGAGGGCAACAGCGGCCGGCAGAAG 60  
Db 7 ATGGCCcAGGGATGGATGTTGATAACCCGAGGGCAACAGCGGCCGGCAGAAG 66

Qy 61 CGCTTGAAGTGAAGAAAGTGGAAATGCGTAAGCTGGGCTGGGATATTGTGGTTGAT 120  
Db 67 CGCTTGAAGTGAAGAAAGTGGAAATGCGTAAGCTGGGCTGGGATATTGTGGTTGAT 126

Qy 121 AACTGTCCCATCTGCAAGAACACATTATGATTCATGATAAGTCAAGCTAACAG 180  
Db 127 AACTGTCCCATCTGCAAGAACACATTATGATTCATGATAAGTCAAGCTAACAG 186

Qy 181 GCGTCCGCTACTTCAGAAGAGTGACTGTCGATGGGAGTCTGTAACCATGTTTAC 240  
Db 187 GCGTCCGCTACTTCAGAAGAGTGACTGTCGATGGGAGTCTGTAACCATGTTTAC 246

Qy 241 TTCCACTGCACTCTCGTGGCTCAAACAGACAGTGTCATGGGCTATTGGACAAAGAG 300  
Db 247 TTCCACTGCACTCTCGTGGCTCAAACAGACAGTGTCATGGGCTATTGGACAAAGAG 306

Qy 301 TGGGAATTCAAAAGTATGGGCACTAG 327  
Db 307 TGGGAATTCAAAAGTATGGGCACTAG 333

RESULT 4  
LOCUS BG77485 488 bp mRNA linear EST 15-MAY-2001  
DEFINITION 606648-0/F1 NIH\_MGC\_60 Homo sapiens cDNA clone IMAGE:4804661 5', mRNA sequence.

ORGANISM Homo sapiens (human)

KEYWORD Unpublished (1999)  
COMMENT Contact: Robert Straussberg, Ph.D.  
Email: cgabro-r@mail.nih.gov  
Tissue Procurement: DCND/DRP  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILINL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
http://image.llnl.gov  
Plate: LLM151 row: h column: 06  
High quality sequence stop: 487.  
Source 1. 488 /organism="Homo sapiens"

FEATURES /mol type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4804661"  
/tissue\_type="adenocarcinoma"

/lab\_host="DH10B (r1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_60"  
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
Site 1: SfiI (ggccgcctggcc); Site 2: SfiI (ggccatattggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3'; and 3' adaptor sequence:  
5'-ATTCTAGAGGGAGGGGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-1.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query	Match	Score	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	1 ATGGCCcAGGGATGGATGTTGATAACCCGAGGGCAACAGCGGCCGGCAGAAG 60	100.0%	327	DB 2	100.0%	0	0	0
Db	23 ATGGCCcAGGGATGGATGTTGATAACCCGAGGGCAACAGCGGCCGGCAGAAG 82	100.0%	327	DB 1	100.0%	0	0	0
Qy	61 CGCTTGAAGTGAAGAAAGTGGAAATGCGTAAGCTGGGATATTGTGGTTGAT 120	97.0%	327	Qy	100.0%	0	0	0
Db	63 CGCTTGAAGTGAAGAAAGTGGAAATGCGTAAGCTGGGATATTGTGGTTGAT 126	97.0%	327	Db	100.0%	0	0	0
Qy	121 AACTGTCCCATCTGCAAGAACACATTATGATTCATGATAAGTCAAGCTAACAG 180	97.0%	327	Qy	100.0%	0	0	0
Db	127 AACTGTCCCATCTGCAAGAACACATTATGATTCATGATAAGTCAAGCTAACAG 186	97.0%	327	Db	100.0%	0	0	0
Qy	181 GCGTCCGCTACTTCAGAAGAGTGACTGTCGATGGGAGTCTGTAACCATGTTTAC 240	97.0%	327	Qy	100.0%	0	0	0
Db	187 GCGTCCGCTACTTCAGAAGAGTGACTGTCGATGGGAGTCTGTAACCATGTTTAC 246	97.0%	327	Db	100.0%	0	0	0
Qy	241 TTCCACTGCACTCTCGTGGCTCAAACAGACAGTGTCATGGGCTATTGGACAAAGAG 300	97.0%	327	Qy	100.0%	0	0	0
Db	247 TTCCACTGCACTCTCGTGGCTCAAACAGACAGTGTCATGGGCTATTGGACAAAGAG 306	97.0%	327	Db	100.0%	0	0	0
Qy	301 TGGGAATTCAAAAGTATGGGCACTAG 327	97.0%	327	Qy	100.0%	0	0	0
Db	307 TGGGAATTCAAAAGTATGGGCACTAG 333	97.0%	327	Db	100.0%	0	0	0
RESULT 5				DEFINITION	12B22006_rev_1_C10_r_082_ab1 Chimpanzee brain library Koos Pan troglodytes cDNA clone 12B22006_rev_1_C10_r_082.ab1 5', mRNA sequence.			
LOCUS	CB29618	498 bp	mRNA	ACCESSION	CB29618			
DEFINITION	EST		linear	VERSION	CB29618			
KEYWORDS			EST 28-FEB-2003	SOURCE	CB29618			
ORGANISM				ORGANISM	CB29618			
KEYWORD				REFERENCE	CB29618			
COMMENT				AUTHORS	CB29618			
JOURNAL				TITLE	CB29618			
VERSION				JOURNAL	CB29618			
KEYWORD				COMMENT	CB29618			
ORGANISM				COMMENT	CB29618			
KEYWORD				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29618			
REFERENCE				COMMENT	CB29618			
AUTHORS				COMMENT	CB29618			
TITLE				COMMENT	CB29618			
JOURNAL				COMMENT	CB29618			
COMMENT				COMMENT	CB29			

FEATURES source	Location/Qualifiers 1. .498 /organism="Pan troglodytes" /mol_type="mRNA" /db_xref="taxon:9598" /clone_id="12822006_rev_1_C10_r_082.ab1" /sex="male" /tissue_type="brain, presumably cortex" /dev_stage="adult" /lab_host="Epicurian Coli (TM) XL-10-Gold" /clone_lib="Chimpanzee brain library Koos" /note=vector: plChi; Site 1: SfiI-A; Site 2: SfiI-B; The library was prepared using the SMART cDNA Library construction kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocol was that we cloned the cDNA into a plasmid vector."	Fax: 650 473 7760 Email: tbrandenberger@geron.com Insert Length: 509 Std Error: 0.00. Location/Qualifiers 1..509 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="axon:9606" /tissue_type="embryonic stem cell, retinoic acid and mitogen-treated HEK cell line H7" /clone_lib="GRN PRENEU" /note="Oligo dT Primed, full-length enriched cDNA library from hES cell line H7 (p28) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic acid and mitogens."
ORIGIN	Query Match 100.0%; Score 327; DB 6; Length 498; Best Local Similarity 100.0%; Pred. No. 6..6e-175; Mismatches 0; Indels 0; Gaps 0; Matches 327; Conservative 0; MisMatches 0; Gaps 0;	Query Match 100.0%; Score 327; DB 7; Length 509; Best Local Similarity 100.0%; Pred. No. 6..6e-175; Mismatches 0; Indels 0; Gaps 0; Matches 327; Conservative 0; MisMatches 0; Gaps 0;
Qy	1 ATGGCGCACCGATGGATGGATGTTGGATACCCCGAGGGCACCAACAGGCCGGGAAGAG 60 2 ATGGCGCACCGATGGATGGATGGATACCCCGAGGGCACCAACAGGCCGGGAAGAG 61	Qy 1 ATGGCGCACCGATGGATGGATGTTGGATACCCCGAGGGCACCAACAGGCCGGGAAGAG 60 6 ATGGCGCACCGATGGATGGATACCCCGAGGGCACCAACAGGCCGGGAAGAG 65
Db	61 CGCTTGAACTGAAAGTGTGAAATGCTGAAATGAGCCCTCTGGCATGGATTGGTGTGAT 120 62 CGCTTGAACTGAAAGTGTGAAATGAGCTGAACTGAGCCCTCTGGCATGGATTGGTGTGAT 121	Qy 61 CGCTTGAACTGAAAGTGTGAAATGAGCCCTCTGGCATGGATTGGTGTGAT 120 66 CGCTTGAACTGAAAGTGTGAAATGAGCCCTCTGGCATGGATTGGTGTGAT 125
Qy	121 AACATGCCATTCAGAACCAATTATGGATTTGGATGAAATGTAAGCTAACCGTAACCG 180 122 AACATGCCATTCAGAACCAATTATGGATCTTGATAGAATGTAAGCTAACCGTAACCG 181	Qy 121 AACATGCCATTCAGAACCAATTATGGATTTGGATGAAATGTAAGCTAACCGTAACCG 180 181 CGCTCGCTACTTCAGAACAGTGTACTGCTGCACTGGGACTCTGTAAACCATGCTTTAAC 240
Db	182 GCGTCGCTACTTCAGAACAGTGTACTGCTGCACTGGGACTCTGTAAACCATGCTTTAAC 241 183 TTCCACTGCATCTCTGCTGCTCAAACACAGCACAGGTGTCTGCTGCTGCTGCTGCTGCTG 300	Db 182 GCGTCGCTACTTCAGAACAGTGTACTGCTGCACTGGGACTCTGTAAACCATGCTTTAAC 241 241 TTCCACTGCATCTCTGCTGCTGCTCAAACACAGCACAGGTGTCTGCTGCTGCTGCTGCTG 300
Qy	241 TTCCACTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301 242 TTCCACTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301	Db 241 TTCCACTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301 246 TTCCACTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 305
Qy	301 TGGAAATTCCAAGATAAGTGGCACTAG 327 302 TGGAAATTCCAAGATAAGTGGCACTAG 328	Qy 301 TGGAAATTCCAAGATAAGTGGCACTAG 327 306 TGGAAATTCCAAGATAAGTGGCACTAG 332
Db		RESULT 7 BP420485 LOCUS BP420485 Homo sapiens mRNA linear EST 27-MAY-2005 DEFINITION BP420485 Homo sapiens small intestine Homo sapiens cDNA clone RHE3775r 3', mRNA sequence.
		ACCESSION BP420485 VERSION BP420485 KEYWORDS EST. SOURCE SOURCE Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 518) COMMENT Takeda,J., Jin,L. and Horikawa,Y. Unpublished (2005) Contact: Yukio Horikawa Laboratory of Molecular and Cellular Genetics Institute for Cell, Molecular and Cellular Regulation, Gunma University Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan Tel: 81-27-220-8832 Fax: 81-27-220-8839 Email: yhorikawa@showa.gunma-u.ac.jp. Location/Qualifiers 1..518 /organism="Homo sapiens"
RESULT 6 CN305892	509 bp mRNA Homo sapiens CDNA 5', mRNA sequence.	FEATURES source
LOCUS CN305892	17000600185586 GRN_PRENEU	
DEFINITION		
ACCESSION CN305892		
VERSION CN205892..1		
KEYWORDS EST.		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.		
REFERENCE Li,Y., Xu,C., Fang,R., Guegler,X., Rao,M.S., Mandalam,R., Lebkowski,J. and Stanton,L.W.		
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation		
JOURNAL Nat. Biotechnol.	22 (6), 707-716 (2004)	
PUBLISHER		
COMMENT Contact: Brandenberger R Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658		

```

/mol type="mRNA"
/db_xref="taxon: 9606"
/clone="HB03775r"
/tissue type="small intestine"
/clone_lib="Homo sapiens small intestine"

ORIGIN
Query Match 100.0%; Score 327; DB 3'; Length 518;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

Qy 1 ATGGCGCAGCGCATGGATGGATGGATAACCCGAGCGGCCAACAGCGGGGACCAACAGCGGGGGCAAGAAG 60
Db 14 ATGGCGCAGCGATGGATGGATGGATGGATGGCGAACAGCGGGGAAAG 73
Qy 61 CGCTTGAATGAAAGTGAATGAGTAGACCCCTGGGCTGGATAATGGGTGAT 120
Db 74 CGCTTGAATGAAAGTGAATGGATGGATGGATGGCGCTGGGCTGGATAATGGGTGAT 133
Qy 121 AACGTGCCATCTGCAGAACACATATGGATCTTGATAGAATGCAAGCTAACAG 180
Db 134 AACGTGCCATCTGCAGAACACATATGGATCTTGATAGAATGCAAGCTAACAG 193
Qy 181 GGTCCTACTCTAGAGAGTGTACTCTGGAGCTGTGAAATTGCTTTAAC 240
Db 194 GGTCCTACTCTAGAGAGTGTACTCTGGAGCTGTGAAATTGCTTTAAC 253
Qy 241 TTCCACTGCATCTCTGGCTCAAACACAGCTGGCAATTGGCAACAGAG 300
Db 254 TTCCACTGCATCTCTGGCTCAAACACAGCTGGCAATTGGCAACAGAG 313
Qy 301 TGGGAATTCAAAAGTATGGCACATAG 327
Db 314 TGGGAATTCAAAAGTATGGCACATAG 340

```

```

RESULT 8
AL711573 AL711573 522 bp mRNA linear EST 04-SEP-2003
LOCUS DEFINITION DKFZp686I0483_r1_686 (synonym: h1cc3) Homo sapiens cDNA clone
DEFINITION DKFZp686I0483_5', mRNA sequence.
ACCESSION AL711573
VERSION AL711573.1 GI:19694928
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo
1 (bases 1 to 522)
Koehler, K., Beyer, A., Newes, W., Weil, B. and Wiemann, S.
EST (Koehler, K., Beyer, A., Newes, W., Weil, B. and Wiemann, S.)
Unpublished (1999)
Contact: MIPS

```

Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert.  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No 81 sequence available.  
This clone (DKFZp686I0483) is available at the RZPD in Berlin.  
Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
Source
1. 522
/organism="Homo sapiens"
/mol type="mRNA"
/db\_xref="taxon:9606"
/tissue type="leiomyosarcoma cell line"
/db\_href="DH10B (phage-resistant)"
/clone lib="NTH MGIC 46"
/note="Organ: uterus; Vector: pOTB7; Site\_1: XbaI; Site\_2: dev\_stage="adult"

```

/mol type="mRNA"
/db_xref="taxon: 9606"
/clone="HB03775r"
/tissue type="small intestine"
/clone_lib="Homo sapiens small intestine"

ORIGIN
Query Match 100.0%; Score 327; DB 1'; Length 522;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Indels 0;

Qy 1 ATGGCGCAGCGATGGATGGATGGATAACCCGAGCGGCCAACAGCGGGGGCAAGAAG 60
Db 21 ATGGCGCAGCGATGGATGGATGGATAACCCGAGCGGCCAACAGCGGGGGCAAGAAG 80
Qy 61 CGCTTGAATGAAAGTGAATGAGTAGACCCCTGGGCTGGATAATGGGTGAT 120
Db 81 CGCTTGAATGAAAGTGAATGAGTAGACCCCTGGGCTGGATAATGGGTGAT 140
Qy 121 AACGTGCCATCTGCAGAACACATATGGATCTTGATAGAATGCAAGCTAACAG 180
Db 141 AACGTGCCATCTGCAGAACACATATGGATCTTGATAGAATGCAAGCTAACAG 200
Qy 181 GGTCCTACTCTAGAGAGTGTACTCTGGAGCTGTGAAATTGCTTTAAC 240
Db 201 GGTCCTACTCTAGAGACTGTACTCTGGAGCTGTGAAATTGCTTTAAC 260
Qy 241 TTCCACTGCATCTCTGGCTCAAACACAGCTGGCAATTGGCAACAGAG 300
Db 261 TTCCACTGCATCTCTGGCTCAAACACAGCTGGCAATTGGCAACAGAG 320
Qy 301 TGGGAATTCAAAAGTATGGCACATAG 327
Db 321 TGGGAATTCAAAAGTATGGCACATAG 347

RESULT 9
BG337472 BG337472 525 bp mRNA linear EST 27-FEB-2001
LOCUS DEFINITION 602435003F1 NIH MGIC 46 Homo sapiens cDNA clone IMAGE 4553064 5',
mRNA sequence.
ACCESSION BG337472
VERSION BG337472.1 GI:13143910
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo
1 (bases 1 to 525)
NIH-MGC http://mgc.nci.nih.gov/
TITLE Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Straubberg, Ph.D.
Email: cgsph@rmal.nih.gov
Tissue Procurement: AMCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Incyte Genomics Inc.
Clone Distribution: MGIC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at:
http://image.lilnl.gov
Plate: LILNL250 row: e column: 01
High quality sequence stop: 525.
Location/Qualifiers
1. 525
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/tissue type="leiomyosarcoma cell line"
/clone lib="NTH MGIC 46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XbaI; Site_2:
```

EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCGAGG(G). Size-selected >500bp for average insert size 1.1-8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

DRIGIN

Query Match	100.0%	Score 327;	DB 2;	Length 525;
Best Local Similarity	100.0%	Pred. No. 6.6e-175;		
Matches	327;	Mismatches	0;	
Dy				
Db	1	ATGCCGGCCGCATGGATGCGATTCGCCAGGGCACCACAGCCGGCGGGCAAGAAG 60		
Db	7	ATGCCGGCCGCATGGATGCGATACCCGAGGGCACCACAGCCGGCGGGCAAGAAG 66		
Dy	61	CGGTTTGAACTGAAAGTGAATGAGTAGCCCTGGCTGGATATTGGTTGAT 120		
Db	67	CGCTTGTGACTGAAAGTGGAAATGGAGTAGCCCTGGCTGGATATTGGTTGAT 126		
Dy	121	AACTGTGCCATCTGAGGAACCAATTGGATCTTGATAGAACTTCAGGTAACCAAG 180		
Db	127	AACTGTGCCATCTGAGGAACCAATTGGATCTTGATAGAACTTCAGGTAACCAAG 186		
Dy	181	GCGTCCGGTACTTCAGAAGAGTGTACTGTGCGCATGGGAGCTGTAAACCATGCTTTCAC 240		
Db	187	GCGTCCGGTACTTCAGAAGAGTGTACTGTGCCATGGGAGCTGTAAACCATGCTTTCAC 246		

Dy	24.1	TTCCAACTGCAATCTCGCTCAAAACAGCAGTGTCCATTGGACACAGAGAG	300
Db	24.7	TTCCAACTGCAATCTCGCTCAAAACAGCAGTGTCCATTGGACACAGAGAG	306
Dy	30.1	TGGGAATTCAAAGATGGGCACTAG	327
Db	30.7	TGGGAATTCAAAGATGGGCACTAG	333

**RESULT 10**  
**LOCUS** BM715215 527 bp mRNA linear EST 28-FEB-2002  
**DEFINITION** UI-E-CL1-af1-h-19-0-UI\_r2 UI-E-CL1 Homo sapiens cDNA clone.  
**ACCESSION** BM715215  
**VERSION** BM715215.1 GI:19028473  
**KEYWORDS** EST  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**MATERIAL** Chordata; Vertebrata; Euteleostomi;  
**MATERIAL** Mammalia; Eutheria; Bimacromyli; Primates; Catarrhini;  
**MATERIAL**

REFERENCE AUTHORS TITLE

Bonato, M.P., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
expression analysis in *Homo sapiens*. *Homology*, 1996, 12, 521-527.

JOURNAL **Genome Res.** 6 (9), 791-806 (1996)  
PUBMED 888548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
215 Newton Road 4156 MRRII Iowa City IA 52242 USA

3535 Neki Rd., Iowa City, IA 52242  
Tel.: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arranged by: Dr. M. Bento Soares, University of Iowa  
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Research Genetics ([www.resgen.com](http://www.resgen.com)).  
Seq Primer: M13 Reverse.

source

1. .527  
 /organism="Homo sapiens"  
 /mol type="mRNA"  
 /db\_Xref="taxon: 9606"  
 /clone="UTI-E-CL1-ati-h-19-0-UII"  
 /tissue type="human retina"  
 /dev\_stage="adult"  
 /lab\_hob="DHL0B (Life Technologies)  
 /clone\_lab="UTI-E-CL1"  
 /note="Organ: eye; Vector: pRT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UTI-E-CL1 is a normalized cDNA library containing the following tissue(s): retina. The library was constructed according to Bonaldo, Lennon and Soares. Genome Research, 6: 791-805, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGCG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

Score 327; DB 3; Length 527;  
Pred. No. 6.6e-175;  
Mismatches 0; Indels 0

TCCAAAGTATGGCACTAG 327.  
 |||||  
 TCCAAAGTATGGCACTAG 330

R\_10473929 NIH\_MGC\_127 Homo sapiens cDNA clone EST 18-OCT-2002

Lens (human)  
Lens  
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Hominidae; Homo.  
1 to 527)  
<http://mgc.nci.nih.gov/>.  
Institutes of Health, Mammalian Gene Collection (MGC)  
Robert Straussberg, Ph.D.  
13337 5', mRNA sequence.

卷之三

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: NCI  
cDNA Library Preparation: Michael Brownstein Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution by: Agencourt Bioscience Corporation  
found through the I.M.A.G.E. Consortium information can be  
http://image.llnl.gov

Plate: LNCM295 row: e column: 17  
FEATURES  
Source  
1. .527  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6673337"  
/tissue\_type="mixed (pool of 40 RNAs)"  
/lab\_host="DH10B (T1-phage-resistant)"  
/clone\_lib="NIH MGC 127"  
/notes="Vector: PDR-LIB; Site\_1: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33 4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.3%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:  
5'-AAGCCATGGCTATCAAGCAGACGCGCATTAACGGCGG-3'  
5'-ATTCTAGGGCGAGGGGAGCTGCGACATGCG-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH MGC 126 and NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC Library."

ORIGIN

Query	Match	Score	Length
Db	Best Local Similarity 100.0%; Pred. No. 6.6e-175; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%	527;
Qy	1 ATGGCCCAAGCGATGGATGTGGATACCCGAGGGGCCAACAGGGGGCAAGAAG 60 24 ATGGCCCAAGCGATGGATGTGGATACCCGAGGGGCCAACAGGGGGCAAGAAG 83		
Db	61 CGCTTAACTGAAAAGTGGATGGTAGGCCCTGGCTGGATTATGGCTTGAT 120 84 CGCTTAACTGAAAAGTGGATGGTAGCTGGCTGGATATGGCTTGAT 143		
Qy	121 AACTRGGCCAATCTGAGGAACCACATTATGGATCTTGGATAGAAATGTAACAG 180 144 AACTGTMCCCATCTGAGGAACCACATTATGGATCTTGGATAGGTACAG 203		
Db	181 GCGTCCCCTACTTCAGAAGTGTACTGTCCTGGAGCTCTGTAACCTTCAC 240 204 GCTGCCCTACTTCAGAAGTGTACTGTCCTGGAGCTCTGTAACCTTCAC 263		
Qy	241 TTCCACTGCACTCTGGCTCAAACAGACAGGTGTCTCATTGGACAACAGAG 300 264 TTCCACTGCACTCTGGCTCAAACAGACAGGTGTCTCATTGGACAACAGAG 323		
Db	301 TGGGAATTCCAAAAGTGGCACTAG 327 324 TGGGAATTCCAAAAGTGGCACTAG 350		

RESULT 12  
CB999822 LOCUS CB999822  
DEFINITION AGENCOURT 13645988 NIH MGC 186 Homo sapiens cDNA clone IMAGE:30322649 5', mRNA sequence.  
ACCESSION CB999822

VERSION CB999822.1 GI:30294342  
EST Homo sapiens (human)  
KEYWORD Homo sapiens  
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Hominoidea; Homo  
REFERENCE 1 (bases 1 to 527)  
AUTHORS NIH-MGC http://mhc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Straubberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution by: Agencourt Bioscience Corporation  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: NDCM123 row: P column: 18  
High quality sequence stop: 518.  
FEATURES  
source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30322649"  
/label="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH MGC 186"  
/notes="Vector: pDNR-LIB; Site\_1: SfiI (ggccgttggcc); Library is oligo-dt primed and directionally cloned. cDNA was prepared from a pooled samples of tissues from Skin, meninges, duramater, pia matter and choroid plexus, and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGGGCGAGCTGCG-3' (30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library"

ORIGIN

Query	Match	Score	Length
Qy	1 ATGGCCCAAGCGATGGATGTGGATACCCGAGGGGCCAACAGGGGGCAAGAAG 60 24 ATGGCCCAAGCGATGGATGTGGATACCCGAGGGGCCAACAGGGGGCAAGAAG 83	100.0%	527;
Db	61 CGCTTAACTGAAAAGTGGATGGTAGGCCCTGGCTGGATTATGGCTTGAT 120 84 CGCTTAACTGAAAAGTGGATGGTAGCTGGCTGGATATGGCTTGAT 143	100.0%	527;
Qy	121 AACTRGGCCAATCTGAGGAACCACATTATGGATCTTGGATAGAAATGTAACAG 180 144 AACTGTMCCCATCTGAGGAACCACATTATGGATCTTGGATAGGTACAG 203	100.0%	527;
Db	181 GCGTCCCCTACTTCAGAAGTGTACTGTCCTGGAGCTCTGTAACCTTCAC 240 204 GCTGCCCTACTTCAGAAGTGTACTGTCCTGGAGCTCTGTAACCTTCAC 263	100.0%	527;
Qy	241 TTCCACTGCACTCTGGCTCAAACAGACAGGTGTCTCATTGGACAACAGAG 300 264 TTCCACTGCACTCTGGCTCAAACAGACAGGTGTCTCATTGGACAACAGAG 323	100.0%	527;
Db	301 TGGGAATTCCAAAAGTGGCACTAG 327 324 TGGGAATTCCAAAAGTGGCACTAG 350	100.0%	527;

Query Match Score 327; DB 6; Length 527;  
Best Local Similarity 100.0%; Pred. No. 6.6e-175; Mismatches 0; N mismatches 0; Indels 0; Gaps 0;  
Matches 327; Conservative 0; Insertions 0; Deletions 0;  
Qy 1 ATGGCCCAAGCGATGGATGTGGATACCCGAGGGGCCAACAGGGGGCAAGAAG 60  
Db 25 ATGGCCCAAGCGATGGATGTGGATACCCGAGGGGCCAACAGGGGGCAAGAAG 84  
Qy 61 CGCTTAACTGAAAAGTGGATGGTAGGCCCTGGCTGGATTATGGCTTGAT 120  
Db 61 CGCTTAACTGAAAAGTGGATGGTAGCTGGCTGGATTATGGCTTGAT 144  
Qy 85 CGCTTAACTGAAAAGTGGATGGTAGCTGGCTGGATTATGGCTTGAT 144  
Db 121 AACTRGGCCAATCTGAGGAACCACATTATGGATCTTGGATAGAAATGTAACAG 180  
Db 145 AACTRGGCCAATCTGAGGAACCACATTATGGATCTTGGATAGAAATGTAACAG 204  
Qy 181 GCGTCCCCTACTTCAGAAGTGTACTGTCCTGGAGCTCTGTAACCTTCAC 240  
Db 181 GCGTCCCCTACTTCAGAAGTGTACTGTCCTGGAGCTCTGTAACCTTCAC 240  
Qy 241 TTCCACTGCACTCTGGCTCAAACAGACAGGTGTCTCATTGGACAACAGAG 300  
Db 205 GCGTCCCCTACTTCAGAAGTGTACTGTCCTGGAGCTCTGTAACCTTCAC 264  
Qy 241 TTCCACTGCACTCTGGCTCAAACAGACAGGTGTCTCATTGGACAACAGAG 300  
Db 265 TTCCACTGCACTCTGGCTCAAACAGACAGGTGTCTCATTGGACAACAGAG 324  
Qy 301 TGGGAATTCCAAAAGTGGCACTAG 327  
Db 325 TGGGAATTCCAAAAGTGGCACTAG 351

RESULT 13	BM757406	mRNA	linear	EST 04-MAR-2002
DEFINITION	K-ESTR003-388	S1SN5 Homo sapiens cDNA clone S1SN5-29-H12 5'	, mRNA sequence.	
ACCESSION	BM757406	529 bp		
VERSION	BM757406..1			
EST.	GI:19087021			
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo;			
REFERENCE	1 (bases 1 to 529)	RESULT 14		
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Kim,Y.S.	CD523457	531 bp	mRNA, linear EST 06-JUN-2003
TITLE	21C Frontier Korean EST Project 2001	LOCUS	AGENCOURT 14360071 NIH MGC 191	Homo sapiens cDNA clone
JOURNAL	Unpublished (2002)	DEFINITION	IMAGE 30472182 5', mRNA sequence.	
COMMENT	Contract: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Baeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Place: 29 row: H column: 12 High quality sequence stop: 529.	ACCESSION	CD523457	
FEATURES	Location/Qualifiers	VERSION	CD523457..1	GI:31455175
source	1..529 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="Taxon:9606" /clone_id="S1SN5-29-H12" /sex="F" /tissue_type="Ascites" /cell_type="Lymphoblast-like" /cell_line="SNU-5" /lab_host="topoDF" /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	ORGANISM	Homo sapiens (human)	
source		REFERENCE	1..531	
		AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/	
		TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
		COMMENT	Unpublished (1999) Contact: Daniel S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A7 Bethesda, MD 20892 Email: cgabbs@mail.nih.gov	
		FEATURES	Tissue Preparation: Narayan Bhattacharya; ClONTECH Laboratories, Inc. CDNA Library Preparation: ClONTECH Laboratories, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LNLL at: http://image.llnl.gov	
		source	Plate: NDCM205 row: C column: 07	
			High quality sequence stop: 518.	
			Location/Qualifiers	
			/organism="Homo sapiens" /mol_type="mRNA" /db_xref="Taxon:9606" /clone_id="S1SN5-29-H12" /note="Vector: pCR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgcctggcc); Library is oligo-3' primed and directionally cloned. pBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA dn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCCCATATGGCC-3', and 3' adaptor sequence: 5'-ATTCTGAGCCGCGACATG-3'(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb), 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."	
				Query Match Score 327; DB 3; Length 529;
				Best Local Similarity 100.0%; Pred No. 6 6e-175; Indels 0; Gaps 0;
				Matches 327; Conservative 0; Mismatches 0;
Qy	1 ATGGCCGAGCGATGGATGGATAACCCGAGGGCACCAACGGGGCGGGCAAGAG 60			
Db	33 ATGGCCGAGCGATGGATGGATAACCCGAGGGCACCAACGGGGCGGGAAAGAG 92			
Qy	61 CGCTTGAAAGTGAAGTGAATGCAATGCGCTGGATATTGCGTTGAT 120			
Db	93 CGCTTGAAAGTGAAGTGAAGTGAATGCAATGCGCTGGATATTGCGTTGAT 152			
				Query Match Score 327; DB 6; Length 531;
				Best Local Similarity 100.0%; Pred. No. 6.e-175;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGGCGGAGCATGGATGGCTACCCGAGGCCAACAGGGCGGGCAAGAAAG 60

Db 23 ATGGCGGAGCATGGATGGCTACCCGAGGCCAACAGGGCGGGCAAGAAAG 82

Oy 61 CGCTTGAAGTCAAAGTGGAAATGGCTGGATAATGGCTGTGAT 120

Db 83 CGCTTGAAGTCAAAGTGGAAATGGCTGGATAATGGCTGTGAT 142

Oy 121 AACTGTCCATCTGCAGAACCATATGGATCTTCATAGAATGTCAGCTAACACAG 180

Db 143 AACTGTCCATCTGCAGAACCATATGGATCTTCATAGAATGTCAGCTAACACAG 202

Oy 181 GGTTCCCTACTTCAGAGTAGTGACTGTGATGGAGATCTGTAAACATGCTTTAC 240

Db 203 GGTTCCCTACTTCAGAGTAGTGACTGTGATGGAGATCTGTAAACATGCTTTAC 262

OY 241 TTCCACTGCACTCTCCTGGCTCAAAACACAGCTGGTCTCCATTGGACAACAGAGAG 300

Db 263 TTCCACTGCACTCTCCTGGCTCAAAACACAGCTGGTCTCCATTGGACAACAGAGAG 322

Oy 301 TGGGAATTCCTAAAAGTATGGGCACTAG 327

Db 323 TGGGAATTCCTAAAAGTATGGGCACTAG 349

RESULT 15  
BU729963/c  
LOCUS BU729963 533 bp mRNA linear EST 09-OCT-2002  
DEFINITION UI-E-CK1-af1-h-19-0-UI s1 UI-E-CK1 Homo sapiens cDNA clone  
VERSION BU729963.1 GI: 236533376  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 533).  
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery.  
Genome Res. 6 (9), 791-806 (1996)

JOURNAL Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics ([www.resgen.com](http://www.resgen.com)).  
Seq primer: M13 FORWARD  
POLY=A Yes.

FEATURES Location/Qualifiers  
source 1..533  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-CK1-af1-h-19-0-UI"  
/tissue\_type="Retina Foveal and Macular"  
/dev\_stage="Retina"  
/lab\_host="DHIOB (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-CK1"  
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoRI I; Site\_2: Not I;

UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adapter, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG LIB=UI-E-CK1  
TAG SEQ=GTCC"

ORIGIN

	Query	Match	Score	DB	Length
	Best	Local Similarity	100.0%	5	533;
	Matches	Conservative	100.0%	Pred. No.	6..175;
		Mismatches	0;	Indels	0;
		Gaps	0;		

Qy 1 ATGGCGGAGCATGGATGGCTGGATAACAGGGACCAACAGGGCGGGCAAGAAG 60

Db 518 ATGGCGGAGCATGGATGGCTGGATAACAGGGACCAACAGGGCGGGCAAGAAG 459

Qy 61 CGCTTGAAGTCAAAGTGGAAATGCGGAAATGGCTGGATAATGGCTGTGAT 120

Db 458 CGCTTGAAGTCAAAGTGGAAATGGCTGGATAATGGCTGTGAT 399

Qy 121 AACGTGCCATCTGGAGAACCAATTGGATCTGGATAATGGCTGTGAGCTAACAG 180

Db 398 AACGTGCCATCTGGAGAACCAATTGGATCTGGATAATGGCTGTGAGCTAACAG 339

Qy 181 GCGTCGGCTACTCTGAAGAGTGACTGTGATGGAGCTGGAGCTGGTACCTTCAC 240

Db 338 GCGTCGGCTACTCTGAAGAGTGACTGTGATGGAGCTGGAGCTGGTACCTTCAC 279

Qy 241 TTCACTGCACTCTGGCTGGCTCAAACACGAGCTGGTACCTTCAC 300

Db 278 TTCACTGCACTCTGGCTGGCTCAAACACGAGCTGGTACCTTCAC 219

Qy 301 TGGGATTCCAAAAGTATGGGCACTAG 327

Db 218 TGGGATTCCAAAAGTATGGGCACTAG 192

RESULT 16  
BG478622 537 bp mRNA linear EST 21-MAR-2001  
LOCUS BG478622  
DEFINITION 602525509F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4643619 5', mRNA sequence.  
ACCESSION BG478622  
VERSION BG478622.1 GI:13410901  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteostomi;  
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 537).  
AUTHORS NTH-MGC http://mgc.ncbi.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1998)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: ATCC/DCD/DTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGc clone distribution information can be found through the I.M.A.G.E. Consortium/LNRL at:

http://image.llnl.gov  
 Plate: LiCM1414 row: b column: 04  
 High quality sequence stop: 534.

FEATURES  
 Source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone=IMAGE:4643619"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC\_20"  
 note="Organ: skin; Vector: pORB7; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCAGCGAGGATGTGGATACCCAGGCCAACACGGCCAGAG 60 insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
 ORIGIN  
 Query Match 100.0%; Score 327; DB 2; Length 537;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 19 ATGGCGGCAACGGATGGATCTGGATACCCAGGCCAACACGGCCAGAG 78  
 Qy 61 CGCCTTGAACTGAAAGTGGAATCGATAAGCCCTCTGGCCCTGGATATTGTGGTGTAT 120  
 Db 79 CGCCTTGAACTGAAAGTGGAATCGATAAGCCCTCTGGCCCTGGATATTGTGGTGTAT 138  
 Qy 121 AACTGTGCCATCTGAGAACCACTATTGATGCTAGATGTCAGCTAACGTAACCG 180  
 Db 139 AACTGTGCCATCTGAGAACCACTATTGATGCTAGATGTCAGCTAACCGTAACCG 198  
 Qy 181 GCGTCCGCTAATTCAAGAAGGTGTACTGCTCATGGAGCTGTAAACATTGCTTTAC 240  
 Db 199 GCGTCCGCTACTTCAGAAGGTGTACTGCTCATGGAGCTGTAAACATTGCTTTAC 258  
 Qy 241 TTCCACTGCACTCTCGCTGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 300  
 Db 259 TTCCACTGCACTCTCGCTGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 318  
 Qy 301 TGGGAATTCCAAGATGGCCACTAG 327  
 Db 319 TGGGAATTCCAAGATGGCCACTAG 345  
 RESULT 17  
 BU941262 LOCUS BU941262 545 bp mRNA linear EST 18-OCT-2002  
 DEFINITION AGNCOURT10512526 NIH MGC\_127 Homo sapiens cDNA clone IMAGE:6713348 5', mRNA sequence.  
 ACCESSION BU941262  
 VERSION 1 GI:24130081  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 COMMENT 1 (bases 1 to 545) NIH-MGC http://mgc.ncbi.nih.gov/  
 REFERENCE NIH-MGC  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs:r@mail.nih.gov  
 Tissue Procurement: NCI  
 cDNA Library Preparation: Michael Brownstein Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LiCM3023 row: h column: 20  
 High quality sequence stop: 522.  
 Location/Qualifiers  
 1. .545  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6713348"  
 /tissue\_type="mixed (pool of 40 RNAs)"  
 /lab\_host="DH10B (T1-phage-resistant)"  
 /clone\_lib="NIH MGC\_127"  
 /note="Vector: pBR-N-LIB; Site 1: SfiI (ggccatccggcc); Double stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5', and 3' adaptors were used in cloning as follows: 5'-ATTCATAGCCGGCGGCGACATGCTTGTGATG-3' and 5'-ATTCATAGCCGGCGGCGACATGCTTGTGATG-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size selected to contain the 1-2 kb size fraction (other fractions present in NIH MGC\_126 and NIH MGC\_128). Library created in the laboratory of T. usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC Library."  
 ORIGIN  
 Query Match 100.0%; Score 327; DB 5; Length 545;  
 Best Local Similarity 100.0%; Prod. No. 6.6e-175;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATGGCGCACCCGAGGGATGTGGATACCCAGGCCAACACGGCCAGGGCGGGCGAACAGAG 60  
 Db 32 ATGGCGCACCCGAGGGATGTGGATACCCAGGCCAACACGGCCAGGGCGGGCGAACAGAG 91  
 Qy 61 CGCTTGAACTGAAAGTGGAATCGATAAGCCCTCTGGCCCTGGATATTGTGGTGTAT 120  
 Db 92 CGCTTGAACTGAAAGTGGAATCGATAAGCCCTCTGGCCCTGGATATTGTGGTGTAT 151  
 Qy 121 AACTGTGCCATCTGAGAACCACTATTGATGCTAGATGTCAGCTAACGTAACCG 180  
 Db 152 AACGTGCCATCTGAGAACCACTATTGATGCTAGATGTCAGCTAACGTAACCG 211  
 Qy 181 GCGTGGTACTCTGAGAACCACTATTGATGCTAGATGTCAGCTAACGTAACCG 240  
 Db 212 GCGTGGTACTCTGAGAACCACTATTGATGCTAGATGTCAGCTAACGTAACCG 271  
 Qy 241 TTCCACTGCACTCTCGCTGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 300  
 Db 272 TTCCACTGCACTCTCGCTGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 331  
 Qy 301 TGGGAATTCCAAGATGGCCACTAG 327  
 Db 332 TGGGAATTCCAAGATGGCCACTAG 358  
 RESULT 18  
 BI1198015 LOCUS BI1198015 546 bp mRNA linear EST 10-JUL-2001  
 DEFINITION 60762132F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4897758 5', mRNA sequence.  
 ACCESSION BI1198015  
 VERSION 1 GI:11653036  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo;	SOURCE ORGANISM Homo sapiens Homo sapiens Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo;	Homo sapiens (human)
REFERENCE NIH-MGC 1 (bases 1 to 546) http://mgc.nci.nih.gov/.	REFERENCE 1 (bases 1 to 546) NIH-MGC http://mgc.nci.nih.gov/.	
AUTHORS Unpublished (1999)	AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)	
TITLE Unpublished (1999)	TITLE National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL COMMENT Contact: Robert Straussberg, Ph.D. Email: cgsbps-r@mail.nih.gov	JOURNAL COMMENT Contact: Robert Straussberg, Ph.D. Email: cgsbps-r@mail.nih.gov	
Tissue Procurement: ATCC	Tissue Procurement: NCI	
cDNA Library Preparation: Ling Hong/Rubin Laboratory	cDNA Library Preparation: Michael Brownstein Laboratory	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (L1NL)	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (L1NL)	
DNA Sequencing by: Incyte Genomics, Inc.	DNA Sequencing by: Agencourt Bioscience Corporation	
Clone distribution by: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/L1NL at: image.lnl.gov	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/L1NL at: http://image.lnl.gov	
Plate: L1CM1736 row: o column: 07	Plate: L1CM2672 row: e column: 14	
High quality sequence stop: 525.	High quality sequence stop: 491.	
FEATURES source	FEATURES source	
1. .546 /organism="Homo sapiens" /mol type="mRNA" /db_Xref=taxon:9606" /clone="IMAGE:499758" /tissue type="neuroblastoma" /lab host="DH10B (phage-resistant)" /note="Organ: brain; Vector: pOTB7; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCACGAG (GI). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	1. .546 /organism="Homo sapiens" /mol type="mRNA" /db_Xref=taxon:9606" /clone="IMAGE:16495061" /tissue type="mixed (pool of 40 RNAs)" /lab host="DH10B (T1-phage-resistant)" /note="Vector: pDR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgcctggcc); Double-stranded cDNA was prepared from a pool of 40 cell line poly+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.4%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows: 5' ATTCTAGAGCGCATGGCAGTCAGTGATG-3' and 3' AAAGCTTGTGGATCATGGCAGGGCGACATG-3' (30 NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH_MGC 141). Library created in the laboratory of M. Brownstein (NIHM, NIH). Note: this is a NIH_MGC Library."	
ORIGIN	ORIGIN	
Query Match 100.0%; Score 327; DB 2; Length 546; Best Local Similarity 100.0%; Pred. No. 6.6e-175; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 100.0%; Score 327; DB 5; Length 546; Best Local Similarity 100.0%; Pred. No. 6.6e-175; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 ATGGCCGAGCATGGATGATGAACTTATGATGTTGATGAGAAGCTAACAG 180 Db 18 ATGGCCGAGCATGGATGATGTTGATACCCGAGGGCAAGAG 60 Qy 61 CGCTTTCAGTCAAAGTGGATGAGTGGCTGGGATATTGTGGTGTAT 120 Db 78 CGCTTTCAGTCAAAGTGGATGAGTGGCTGGGATATTGTGGTGTAT 137	Qy 1 ATGGCCGAGCATGGATGATGAACTTATGATGTTGATGAGAAGCTAACAG 180 Db 18 ATGGCCGAGCATGGATGATGTTGATACCCGAGGGCAAGAG 60 Qy 61 CGCTTTCAGTCAAAGTGGATGAGTGGCTGGGATATTGTGGTGTAT 120 Db 78 CGCTTTCAGTCAAAGTGGATGAGTGGCTGGGATATTGTGGTGTAT 137	
Qy 121 AACCTGTCGCAATGTCAGGAACACATTATGATGTTGATGAGAAGCTAACAG 180 Db 138 AACCTGTCGCAATGTCAGGAACACATTATGATGTTGATGAGAAGCTAACAG 197	Qy 121 AACCTGTCGCAATGTCAGGAACACATTATGATGTTGATGAGAAGCTAACAG 180 Db 138 AACCTGTCGCAATGTCAGGAACACATTATGATGTTGATGAGAAGCTAACAG 197	
Qy 181 GCGTCCCTACTTCAGAAGCTGACTGTCGATGGAGCTGTAACATGCTTTCAC 240 Db 198 GCGTCCCTACTTCAGAAGCTGACTGTCGATGGAGCTGTCATGGTAACTGCTTTCAC 257	Qy 181 GCGTCCCTACTTCAGAAGCTGACTGTCGATGGAGCTGTAACATGCTTTCAC 240 Db 198 GCGTCCCTACTTCAGAAGCTGACTGTCGATGGAGCTGTCATGGTAACTGCTTTCAC 257	
Qy 241 TTCCACTGCACTCTCTCTGGTCATAAAACACGACAGTGTCTGGCTCATGGAAACAGAG 300 Db 258 TTCCACTGCACTCTCTCTGGTCATAAAACACGACAGTGTCTGGCTCATGGAAACAGAG 317	Qy 241 TTCCACTGCACTCTCTGGTCATAAAACACGACAGTGTCTGGCTCATGGAAACAGAG 300 Db 258 TTCCACTGCACTCTCTGGTCATAAAACACGACAGTGTCTGGCTCATGGAAACAGAG 317	
Qy 301 TGGGAATTCCAAAAGTGGTGGCACTAG 327 Db 318 TGGGAATTCCAAAAGTGGTGGCACTAG 344	Qy 301 TGGGAATTCCAAAAGTGGTGGCACTAG 327 Db 318 TGGGAATTCCAAAAGTGGTGGCACTAG 344	
RESULT 19 BU601181 LOCUS AGENCOURT 10029786 NIH MGC 142 Homo sapiens cDNA clone DEFINITION IMAGE:6495061 5', mRNA sequence. ACCESSION BU601181 VERSION GI:23252940 KEYWORDS EST.	RESULT 19 BU601181 LOCUS AGENCOURT 10029786 NIH MGC 142 Homo sapiens cDNA clone DEFINITION IMAGE:6495061 5', mRNA sequence. ACCESSION BU601181 VERSION GI:23252940 KEYWORDS EST.	
181 GCGTCCCTACTTCAGAAGCTGACTGTCGATGGAGCTGTAACATGCTTTCAC 240 193 GCGTCCCTACTTCAGAAGCTGACTGTCGATGGAGCTGTCATGGTAACTGCTTTCAC 252 241 TTCCACTGCACTCTCTGGTCATAAAACACGACAGTGTCTGGCTCATGGAAACAGAG 300 253 TTCCACTGCACTCTCTGGTCATAAAACACGACAGTGTCTGGCTCATGGAAACAGAG 312 301 TGGGAATTCCAAAAGTGGTGGCACTAG 327	181 GCGTCCCTACTTCAGAAGCTGACTGTCGATGGAGCTGTAACATGCTTTCAC 240 193 GCGTCCCTACTTCAGAAGCTGACTGTCGATGGAGCTGTCATGGTAACTGCTTTCAC 252 241 TTCCACTGCACTCTCTGGTCATAAAACACGACAGTGTCTGGCTCATGGAAACAGAG 300 253 TTCCACTGCACTCTCTGGTCATAAAACACGACAGTGTCTGGCTCATGGAAACAGAG 312 301 TGGGAATTCCAAAAGTGGTGGCACTAG 327	



Qy	241	TTC CACTGCATCTCGCTGCTCAAACAGACAGGTGTCATTGGACAAGAG 300	Qy	241	TTC CACTGCATCTCGCTGCTCAAACAGACAGGTGTCATTGGACAAGAG 300			
Db	257	TTCCACTGCATCTCGCTGCTCAAACAGACAGGTGTCATTGGACAAGAG 316	Db	241	TTCCACTGCATCTCGCTGCTCAAACAGACAGGTGTCATTGGACAAGAG 300			
Qy	301	TGGGAATTCAAAAGTATGGCCTAG 327	Qy	301	TGGGAATTCAAAAGTATGGCCTAG 327			
Db	317	TGGGAATTCAAAAGTATGGCCTAG 343	Db	301	TGGGAATTCAAAAGTATGGCCTAG 327			
RESULT 22			RESULT 23					
B1858425	BT1858425	549 bp mRNA linear EST 10-OCT-2001	B1858425	BU955646	550 bp mRNA linear EST 21-OCT-2002			
LOCUS	603386437F1	NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5395281 5', mRNA sequence.	LOCUS	AGENCOURT 10612538 NIH_MGC_126 Homo sapiens cDNA clone IMAGE:6727978 5', mRNA sequence.				
DEFINITION			DEFINITION					
ACCESSION	B1858425		ACCESSION	BU955646				
VERSION	BT1858425..1	GI:159991972	VERSION	BU955646..1	GI:24185218			
KEYWORDS			KEYWORDS					
SOURCE	Homo sapiens (human)		SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens		ORGANISM	Homo sapiens				
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.			Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.					
REFERENCE	1	(bases 1 to 549) NIH-MGC http://mgc.nci.nih.gov/	REFERENCE	1	(bases 1 to 550) NIH-MGC http://mgc.nci.nih.gov/			
AUTHORS		National Institutes of Health, Mammalian Gene Collection (MGC)	AUTHORS		National Institutes of Health, Mammalian Gene Collection (MGC)			
TITLE			TITLE					
JOURNAL		Unpublished (1999)	JOURNAL		Unpublished (1999)			
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabps@MAIL.nih.gov	COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabps@MAIL.nih.gov			
Tissue Procurement:	DCRD/DRP	CDNA Library Preparation: Michael Brownstein Laboratory	Tissue Procurement:	DCRD/DRP	CDNA Library Preparation: Michael Brownstein Laboratory			
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LINL)	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)	CDNA Library Arrayed by:	Agencourt Bioscience Corporation	CDNA Library Arrayed by: Agencourt Bioscience Corporation			
DNA Sequencing by:	Incyte Genomics, Inc.	DNA Sequencing by: Agencourt Bioscience Corporation	DNA Sequencing by:		DNA Sequencing by: Agencourt Bioscience Corporation			
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIHL at: http://image.llnl.gov	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIHL at: http://image.llnl.gov	Clone distribution:		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIHL at: http://image.llnl.gov			
Plate:	LLAM1207	row: i column: 10	Plate:	LICM3048	row: j column: 05			
FEATURES		High quality sequence stop: 525.	FEATURES		High quality sequence stop: 520.			
source	1..549	Location/Qualifiers	source	1..550	Location/Qualifiers			
		/organism="Homo sapiens"			/organism="Homo sapiens"			
		/mol_type="mRNA"			/mol_type="mRNA"			
		/db_xref="taxon:9606"			/db_xref="taxon:9606"			
		/clone="IMAGE:5395281"			/clone="IMAGE:6727978"			
		/tissue type="mammary adenocarcinoma, cell line"			/tissue type="mixture (pool of 40 RNAs)"			
		/lab_host="DH10B (phage-resistant)"			/lab_host="DH10B (T1-phage-resistant)"			
		/clone_lib="NIH_MGC_87"			/clone_lib="NIH_MGC_126"			
		/note="Organ: breast" Vector: PCMV-SPORT6; Site 1: NotI;			/note=Vector: PBNR-LIB; Site 1: SfiI (ggccattatggcc);			
		Site 2: SalI; Cloned unidirectionally; oligo-dT primed.			Site 2: SfiI (ggccgcctcgcc); Double-stranded DNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%) 5, and 3' adaptors were used in cloning as follows: 5'-ATTCATAGGCCGAGTCGCATGCCATTACGCCGG-3', and 5'-AAGCACTGCTATCAACGCCAGTCGCATGCCATTACGCCGG-3', and Full-length enriched library was constructed using the Clonetech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Uedin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."			
		Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.						
		Note: this is a NIH_MGC Library."						
ORIGIN			Query Match	100.0%	Score 327; DB 5; Length 549;			
			Best Local Similarity	100.0%	Pred. No. 6..175;			
			Matches	327; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;			
Qy	1	ATGGCGCAGCGATGATGGATACCCSAGCGCCAAAGGGGGAGAG 60	Qy	1	ATGGCGCAGCGATGATGGATACCCSAGCGCCAAAGGGGGAGAG 60			
Db	1	ATGGCGCAGCGATGATGGATACCCSAGCGCCAAAGGGGGAGAG 60	Db	121	AACTGCGCCATCTCGAGAACCATATGATGTCAGTAACCTGCAAC 180			
Qy	61	CGCTTGAACTGAAAGTGAATGGATGCTGGCCCTGGATATTGGTTAT 120	Qy	121	AACTGCGCCATCTCGAGAACCATATGATGTCAGTAACCTGCAAC 180			
Db	61	CGCTTGAACTGAAAGTGAATGGATGCTGGCCCTGGATATTGGTTAT 120	Db	121	AACTGCGCCATCTCGAGAACCATATGATGTCAGTAACCTGCAAC 180			
Qy	181	GCGTCGGCTACTTCAGAAGTGTACTGGCATGGAGTCTGTAACCATGCTTTCAC 240	Qy	181	GCGTCGGCTACTTCAGAAGTGTACTGGCATGGAGTCTGTAACCATGCTTTCAC 240			
Db	181	GCGTCGGCTACTTCAGAAGTGTACTGGCATGGAGTCTGTAACCATGCTTTCAC 240	Db	17	ATGGCGCAGCGATGATGGATACCCSAGCGCCAAAGGGGGAGAG 76			

Qy	61	CGCTTTGAAGTGAAGAAGTGGAAATGCCGTAGCCCTCTGGGATTGGGATATTGGTGTCAAT	120	Qy	61	CGTTTGAAAGTGAAGAAGTGGAAATGCCGTAGCCCTCTGGGATTGGGATATTGGTGTCAAT	120
Db	77	CGCTTTGAAGTGAAGAAGTGGAAATGCCGTAGCCCTCTGGGATTGGTGTCAAT	136	Db	94	CGCTTGAAAGTGAAGAAGTGGAAATGCCGTAGCCCTCTGGGATTGGTGTCAAT	153
Qy	121	AACCTGCCCCATCTCGAGGAAACCAATTAGGATCTTGGATAGATGCAAGCTAACAG	180	Qy	121	AACCTGCCCCATCTCGAGGAAACCAATTAGGATCTTGGATAGATGCAAGCTAACAG	180
Db	137	AACCTGCCCCATCTCGAGGAAACCAATTAGGATCTTGGATAGATGCAAGCTAACAG	196	Db	154	AACCTGCCCCATCTCGAGGAAACCAATTAGGATCTTGGATAGATGCAAGCTAACAG	213
Qy	181	GCGTCGGCTACTTCAGAAAGTGTACTCTGCGATGGGAGTCTGTAACCATGCTTCAAC	240	Qy	181	GCGTCGGCTACTTCAGAAAGTGTACTCTGCGATGGGAGTCTGTAACCATGCTTCAAC	240
Db	197	GCGTCGGCTACTTCAGAAAGTGTACTCTGCGATGGGAGTCTGTAACCATGCTTCAAC	256	Db	214	GCGTCGGCTACTTCAGAAAGTGTACTCTGCGATGGGAGTCTGTAACCATGCTTCAAC	273
Qy	241	TTCGACTGATCTCTCGCTGCTAAAAACAGCACGGTGTCTGATGGACACAGAG	300	Qy	241	TTCGACTGATCTCTCGCTGCTGCTAAAAACAGCACGGTGTCTGATGGACACAGAG	300
Db	257	TTCGACTGATCTCTCGCTGCTGCTAAAAACAGCACGGTGTCTGATGGACACAGAG	316	Db	274	TTCGACTGATCTCTCGCTGCTGCTAAAAACAGCACGGTGTCTGATGGACACAGAG	333
Qy	301	TGGGAATTCCTAAAGATATGGCACTAG	327	Qy	301	TGGGAATTCCTAAAGATATGGCACTAG	327
Db	317	TGGGAATTCCTAAAGATATGGCACTAG	343	Db	334	TGGGAATTCCTAAAGATATGGCACTAG	360
<hr/>							
RESULT 24							
LOCUS	CD249363	554 bp mRNA linear EST 22-MAY-2003		LOCUS	BUS32840	555 bp mRNA linear EST 13-SEP-2002	
DEFINITION	AGENCOURT_14100407 NIH_MGC_172 Homo sapiens cDNA 5'	, mRNA sequence.		DEFINITION	BUS32840	AGENCOURT_10204716 NIH_MGC_126 Homo sapiens cDNA clone	
ACCESSION	CD249363			IMAGE	6558754	, mRNA sequence.	
VERSION	CD249363.1	GI:31009829		ACCESSION	BUS32840		
KEYWORDS	EST.			VERSION	BUS32840.1	GI:22843281	
SOURCE	Homo sapiens (human)			KEYWORDS			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.			SOURCE	Homo sapiens		
REFERENCE	1 (bases 1 to 554)			ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	NIH-MGC	http://mgc.ncbi.nih.gov/		REFERENCE	1 (bases 1 to 554)		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			AUTHORS	NIH-MGC	http://mgc.ncbi.nih.gov/	
JOURNAL	Unpublished (1999)			TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm.0A07 Bethesda, MD 20892 Email: cgabbs@mail.nih.gov			JOURNAL	Unpublished (1999)		
FEATURES	High quality sequence start: 16 High quality sequence stop: 54.			COMMENT	Contact: Robert Strausberg, Ph.D. DNA Sequencing by: Michael Brownstein Laboratory CDNA Library Preparation: Michael Brownstein Laboratory DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
source	Plate: NDKM63 row: p column: 24 High quality sequence start: 16 High quality sequence stop: 54.			FEATURES	Plate: LCM2728 row: o column: 10 High quality sequence stop: 530.		
source	Location/Qualifiers			source	Location/Qualifiers		
1. .554	/organism="Homo sapiens"			1. .555	/organism="Homo sapiens"		
	/mol_type="mRNA"				/mol_type="mRNA"		
	/db_xref="taxon:9606"				/db_xref="taxon:9606"		
	/tissue_type="embryonic stem cells, WA01, passage 38"				/tissue_type="embryonic stem cells, WA01, passage 38"		
	/lab_host="DH10B Tona"				/lab_host="DH10B Tona"		
	/note="Vector: PDONR201; Site 1: attP1; Site 2: attP1; LIBR PRIMING - Oligo dT; METHOD - full-length enriched; Embryonic Stem Cells H1; LIBR PROVIDER - Bradfield"				/note="Vector: PDONR201; Site 1: attP1; Site 2: attP1; LIBR PRIMING - Oligo dT; METHOD - full-length enriched; Embryonic Stem Cells H1; LIBR PROVIDER - Bradfield"		
ORIGIN	Query Match 100.0% Score 327; DB 6; Length 554;			ORIGIN	Query Match 100.0% Score 327; DB 6; Length 554;		
	Best Local Similarity 100.0% Pred. No. 6.6e-175; Mismatches 0; Indels 0; Gaps 0;				Best Local Similarity 100.0% Pred. No. 6.6e-175; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 ATGGCCGCAAGGATGGATGCGATCCCGAGGGCAACAGGGCGGGCAAGAG	60			1 ATGGCCGCAAGGATGGATGCGATCCCGAGGGCAACAGGGCGGGCAAGAG	60	
Db	34 ATGGCCGCAAGGATGGATGCGATCCCGAGGGCAACAGGGCGGGCAAGAG	93			34 ATGGCCGCAAGGATGGATGCGATCCCGAGGGCAACAGGGCGGGCAAGAG	93	

adapters were used in cloning as follows:  
 5'-ATTCTAGGCGGAGGCGGCGGCGCATG-3' and  
 5'-ATTCTAGGCGGAGGCGGCGGCGCATG-3' (NN-3'). Full-length  
 enriched library was constructed using the Clontech  
 Creator SMART kit and size-selected to contain the 0.5-1  
 kb size fraction (other fractions present in NIH\_MGC\_127

and NIH\_MGC\_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIHM, NIH). Note: this is a NIH\_MGC Library."

**ORIGIN**

Query Match	100.0%	Score 327;	DB 5;	Length 555;
Best Local Similarity	100.0%	Pred. No.	6.6e-175;	
Matches	327;	Conservative	0;	Mismatches 0;
				Gaps 0;
Oy	1	ATGGCGCAGCATGGGTGCTGGATAACCCGAGCGGCCAACAGGAG 60		
Db	13	ATGGCGCAGCATGGGTGCTGGATAACCCGAGCGGCCAACAGGAG 72		
Oy	61	CGCTTTCAGTGAAGTGAAGAATGGATGCGTAGCCCTGGCTGGATAATGGTTGAT 120		
Db	73	CGCTTTCAGTGAAGTGAAGAATGGATGCGTAGCCCTGGCTGGATAATGGTTGAT 132		
Oy	121	AACTRGTCGATCTGCAAGAACATATTGATGATCTTGATAGAAATGCTAACAG 180		
Db	133	AACTRGTCGATCTGCAAGAACATATTGATGATCTTGATAGAAATGCTAACAG 192		
Oy	181	GCTGCCCTACTTCAGAGAGTGTCACTGCGATGGGAGTGTCAACCATGCTTAC 240		
Db	193	GCTGCCCTACTTCAGAGAGTGTCACTGCGATGGGAGTGTCAACCATGCTTAC 252		
Oy	241	TTCACATGCATCTCCTGGCTCAAAAACACACAGGTGTCCATTGGACAGAG 300		
Db	253	TTCACATGCATCTCCTGGCTCAAAAACACACAGGTGTCCATTGGACAGAG 312		
Oy	301	TGGAAATTCCAAAAGTATGGGGACTAG 327		
Db	313	TGGAAATTCCAAAAGTATGGGGACTAG 339		

RESULT 26  
BU601080 LOCUS BU601080 555 bp mRNA linear EST 20-SEP-2002  
DEFINITION AGENCOURT 10058991 NIH\_MGC\_42 Homo sapiens cDNA clone IMAGE:6414946 5', mRNA sequence.  
ACCESSION BU601080  
VERSION 1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 555) NIH\_MGC http://mrgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: NCI  
CDNA Library Arrayed by: I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLCM2671 row: P column: 19  
High quality sequence stop: 510.  
Location/Qualifiers

FEATURES 1..555  
Source /organism="Homo sapiens"  
/mol type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6414946"  
/tissue type="mixed (pool of 40 RNAs)"  
/lab\_host="DH40B ("T1-phage-resistant")"  
/clone\_lab="NIH\_MGC\_142"  
/note="Vector: PDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgcctcgcc); Double-stranded CDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, kidney - 1.4%, eye - 1%, intestine - 12.5%, colon - 4%, connective tissue - 1.4%, liver - 5.7%, lung - 10.8%, NK-cell - 2.6%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5, and 3, adaptors were used in cloning as follows:  
5'-ATTCTAGGGTATCAAGCGAGTCGGCCAGCATG-dt (30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH MGC 141). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH\_MGC Library."

ORIGIN Query Match 100.0%; Score 327; DB 5; Length 555;  
Best Local Similarity 100.0%; Pred. No. 6.6e-175;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 ATGGCGCAGCATGGATGCGTAGCCCTGGCTGGATAACAGCGCCGGACCAAGCGCCGGACAGAAG 60  
Db 22 ATGGCGCAGGGATGGATGCGATAACCCGAGCGGCCAACAGCGCCGGACAGAAG 81  
Oy 61 CGCTTTCAGTGAAGTGAAGAAGTGGAAATGCGTAGTGGCTGGATAATGGTTGTAT 120  
Db 82 CGCTTTCAGTGAAGTGAAGAAGTGGAAATGCGTAGTGGCTGGATAATGGTTGTAT 141  
Oy 121 AACGTGGCTACTTCAGAAGAGTGTACTGTCCATGGGAGTCCTGTAAACATGCTTTCAC 240  
Db 202 GCGTCGGCTACTTCAGAAGAGTGTACTGTCCATGGGAGTCCTGTAAACATGCTTTCAC 261  
Oy 241 TTCCACATGCATCTCCTGGCTCAAAAACACACAGGTGTCCATTGGACAGAG 300  
Db 262 TTCCACATGCATCTCCTGGCTCAAAAACACACAGGTGTCCATTGGACAGAG 321  
Oy 301 TGGAAATTCCAAAAGTATGGGGACTAG 327  
Db 322 TGGAAATTCCAAAAGTATGGGGACTAG 348  
RESULT 27  
BU954591 LOCUS BU954591 557 bp mRNA linear EST 21-OCT-2002  
DEFINITION AGENCOURT 10610692 NIH\_MGC\_126 Homo sapiens cDNA clone  
ACCESSION BU954591  
VERSION GI:24184163  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Nounalia; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Hominoidea; Homo.  
COMMENT (bases 1 to 557)  
REFERENCE 1 (bases 1 to 557)  
AUTHORS NIH-MGC http://mrgc.nci.nih.gov/  
TITLE NIH\_MGC IMAGE:6726227 5', mRNA sequence.  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Michael Brownstein Laboratory  
CDNA Library Preparation: Michael Brownstein Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLCM3044 row: e column: 10  
High quality sequence stop: 469.



TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	KEYWORDS	EST, Homo sapiens (human)
JOURNAL	Unpublished (1999)	SOURCE	Homo sapiens
COMMENT	Contact: Daniela S. Gerhard, Ph.D.	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
Office of Cancer Genomics / NIH	Bldg. 31 Rm10A07 Bethesda, MD 20892	REFERENCE	1 (bases 1 to 562)
Email: ceapbs-r@mail.nih.gov	Tissue Procurement: Professor Mikliss Palkovits	AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
Tissue Procurement Preparation: Michael Brownstein / Ted Usdin	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	cDNA Sequencing by: Agencourt Bioscience Corporation	JOURNAL	Unpublished (1999)
DNA Sequencing by: Agencourt Bioscience Corporation	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:	COMMENT	Contact: Robert Strausberg, Ph.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:	http://image.llnl.gov	Email: cgapbs-r@mail.nih.gov	Tissue Procurement: Dr. Jamie Thompson, University of WI
Plate: NCM264 row: n column: 01	Location/Qualifiers	CDNA Library Preparation: Gina Zastrow-Hayes	CDNA Library Arrayed by: Gina Zastrow-Hayes
High quality sequence stop: 543.	1..559	DNA Sequencing by: Agencourt Bioscience Corporation	CDNA Consortium (LNL)
/organism="Homo sapiens"	/mol_type="mRNA"	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:	http://image.llnl.gov
/db_xref=taxon:9606"	/clone="IMAGE:1071940"	Place: NDKM46 row: e column: 05	Place: NDKM46 row: e column: 05
/tissue_type="Human Brain - Cerebellar Cortex"	/tissue_type="Human Brain - Cerebellar Cortex"	High quality sequence start: 28	High quality sequence start: 28
/lab_host="DH10B Tora"	/clone_id="NIH_MGC_228"	High quality sequence stop: 562.	High quality sequence stop: 562.
/clone lib="NIH_MGC_228"	/note="Organ: brain/CNS; Vector: PDNR-LIB; Site 1: SfII (directional); Site 2: SfII (directional); Library is oligo-dT primed and directionally cloned.; 5' and 3'	Location/Qualifiers	Location/Qualifiers
	adaptors were used in cloning as follows: 5'-AGGCAGGGTATAACCCAGACTGGCAATAGCGCGGG-3'5'-ATTCTAGAGGG CCGAGGCCGCGACGT-dT) 3N 1N-2. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected for >0.5kb with an average insert size of 1.2kb. Library created in the laboratory of Jonathan Kuo and Ted Usdin."	1..562	1..562
		/organism="Homo sapiens"	/organism="Homo sapiens"
		/mol_type="mRNA"	/mol_type="mRNA"
		/db_xref=taxon:9606"	/db_xref=taxon:9606"
		/tissue_type="embryonic stem cells, WA01, passage 38"	/tissue_type="embryonic stem cells, WA01, passage 38"
		/lab_host="DH10B Tora"	/lab_host="DH10B Tora"
		/clone lib="NIH_MGC_172"	/clone lib="NIH_MGC_172"
		/note="Vector: PDONR201; Site 1: attP2; Site 2: attP1; LIBR PRIMING - Oligo dT; METHD - full-length enriched Embryonic Stem Cells H1; LIBR PROVIDER - Bradfield"	/note="Vector: PDONR201; Site 1: attP2; Site 2: attP1; LIBR PRIMING - Oligo dT; METHD - full-length enriched Embryonic Stem Cells H1; LIBR PROVIDER - Bradfield"
FEATURES		ORIGIN	ORIGIN
source			
			Query Match 100.0%; Score 327; DB 6; Length 562;
			Best Local Similarity 100.0%; Pred. No. 6..6e-175; Mismatches 0; Indels 0; Gaps 0;
			Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
			Qy 1 ATGGCCGAGGGATGGATGGATACTCCAGCGGCCAACAGCCGCGGCCAGAAAG 60
			Db 23 ATGGCCGAGGGATGGATGGATACTCCAGCGGCCAACAGCCGCGGCCAGAAAG 82
			Qy 61 CGCTTGAAGTGAAGTGAAGTGAATGGAGTAGCCCTCTGGCTGGATATGGTTGAT 120
			Db 83 CGCTTGAAGTGAAGTGAAGTGGATGGATGGATGGCTCTGGCTGGATATGGTTGAT 142
			Qy 121 AACTGTGCCATCTGGAGAACCAATTATGGATCTTGATAGAAATGTCAGCTAACAG 180
			Db 143 AACTGTGCCATCTGGAGAACCAATTATGGATCTTGATAGAAATGTCAGCTAACAG 202
			Qy 181 GGTTCCGCTACTCTGAGAGGTGTACTGCGCATGGAGCTGTAACTGCTTTCAC 240
			Db 203 GGTTCCGCTACTCTGAGAGGTGTACTGCGCATGGAGCTGTAACTGCTTTCAC 262
			Qy 241 TTCCACTGCATCTCTGGCTGGCTCAAACAGGAGCTCATGGACAAACAGAG 300
			Db 263 TTCCACTGCATCTCTGGCTGGCTCAAACAGGAGCTGTAACTGCTTTCAC 322
			Qy 301 TGGGAATTCCAAAAGTGGGACTAG 327
			Db 323 TGGGAATTCCAAAAGTGGGACTAG 349
			Qy 340 TGGGAATTCCAAAAGTGGGACTAG 366
			RESULT 31
			BUB61191
			LOCUS
			DEFINITION
			AGENCOURT_13976103 NIH_MGC_172 Homo sapiens mRNA sequence.
			VERSION
			CD175085_1 GI:24046183
			VERSION
			CD175085_1 GI:30859303
			RESULT 30
			CD175085
			LOCUS
			DEFINITION
			AGENCOURT_13976103 NIH_MGC_172 Homo sapiens mRNA sequence.
			VERSION
			CD175085_1 GI:30859303

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bacteria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	Db	332 TGGAAATTCCAAGTATGGCACCTAG 358
REFERENCE	1 (bases 1 to 563) NIH-MGC http://mgc.ncbi.nih.gov/	RESULT 32	
AUTHORS	NIH-MGC	BUS97842	570 bp mRNA linear EST 20-SEP-2002
TITLE	National Institutes of Health, Mammalian Gene Collection (Mgc)	LOCUS	NIH_MGC_1142 Homo sapiens cDNA clone IMAGE:6456347
JOURNAL	Unpublished (1999)	DEFINITION	5', mRNA sequence.
COMMENT	Contact: Robert Straubhaar, Ph.D. Email: cgbbs@mail.nih.gov Tissue Procurement: NCI CDNA Library Preparation: Michael Brownstein Laboratory DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov/plate: LLM2901 · row: 9 column: 04	ACCESSION	BUS97842
FEATURES	High quality sequence stop: 531. Location/Qualifiers	VERSION	BUS97842.1 GI:23249601
source	1. organism="Homo sapiens" /mol type="mRNA" /db_xref="taxon:96016" /clone="IMAGE:6632636" /tissue_type="mixed (pool of 40 RNAs)" /lab_host="DR10B (T1-phage-resistant)" /note="Vector: PDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgccggcc); Double-stranded CDNA was prepared from a pool of 40 cell line poly+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5, and 3' adaptors were used in cloning as follows: 5'-ATTCTAGGGATGAAAGTGTAAATGCGCCGGG-3' and 5'-ATTCTAGGGATGAAAGTGTAAATGCGCCGGG-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC Library."	ORGANISM	RESULT 32
	Query Match Score 327; DB 5; Length 563; Best Local Similarity 100.0%; Pred. No. 6.6e-175; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Match	100.0%; Score 327; DB 5; Length 570;
Qy	1 ATGGCCGAGGGATGTTGATACTCCGAGGGCAAGAAG 60	Best Local Similarity 100.0%; Pred. No. 6.6e-175;	
Db	32 ATGGCCGAGGGATGTTGATACTCCGAGGGCAAGAAG 91	Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	61 CGCTTGTAAACTGAAAAAATGGAATGCAATGCCCTGTGGATATTGTGTGTGAT 120	Qy	1 ATGGCCGAGGGATGTTGATACTCCGAGGGCAAGAAG 60
Db	92 CGCTTGTAAACTGAAAAATGGAATGCAATGCCCTGTGGATATTGTGTGTGAT 151	Db	32 ATGGCCGAGGGATGTTGATACTCCGAGGGCAAGAAG 91
Qy	121 AACTGTCCTCATCTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 180	Qy	61 CGCTTGTAAACTGAAAAAGTGGATGCTGCTCTGGCTGGATATTGTGTGTGAT 120
Db	152 AACTGTCCTCATCTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 211	Db	92 CGCTTGTAAACTGAAAAAGTGGATGCTGCTCTGGCTGGATATTGTGTGTGAT 151
Qy	181 GCTTGTAAACTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 240	Qy	121 AACCTGTGCCATCTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 180
Db	212 GCTTGTAAACTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 271	Db	152 AACCTGTGCCATCTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 211
Qy	241 TTCCACTGCACTCTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 300	Qy	121 AACCTGTGCCATCTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 180
Db	272 TTCCACTGCACTCTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 331	Db	152 AACCTGTGCCATCTGCGAGAACACATATGGATCTTGCATAGATGCTAACACAG 211
Qy	301 TGGAAATTCCAAAAGTATGGCCACTAG 327	Qy	

Qy	181	GCGTCCGCTACTCAGAACAGTGTACTCTGCCATGGGAGTCAGTGTAAACCATTGCTTTAC	240	Qy	1	ATGGCGGAAGCGATGGATAACCCGAGGGCACCAAGAGCGGGCGGGCGCAAGAG	60
Db	212	GCGTCCGCTACTCAGAACAGTGTACTCTGCCATGGGAGTCAGTGTAAACCATTGCTTTAC	271	Db	38	ATGGCGGAAGCGATGGATAACCCGAGGGCACCAAGAGCGGGCGGGCGCAAGAG	97
Qy	241	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	300	Qy	61	CGGTTGAAGTGAAGAAAGTGGATGAGTAGGCCTCTGGCGGGGATATTGGTTGAT	120
Db	272	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	331	Db	98	CGGTTGAAGTGAAGAAACTGGATGAGTAGGCCTCTGGCGGGATATTGGTTGAT	157
Qy	301	TGGGAATTCCAATGAGTATGGCACTAG	327	Qy	121	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	180
Db	332	TGGGAATTCCAATGAGTATGGCACTAG	358	Db	158	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	217
<b>RESULT 33</b>							
BU533405	BU533405	573 bp mRNA linear EST 13-SEP-2002		Qy	181	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	240
LOCUS	AGENCOURT_10197885	NIH_MGC_126 Homo sapiens cDNA clone		Db	218	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	277
DEFINITION	IMAGE:6555746 5'	mRNA sequence.		Qy	241	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	300
ACCESSION	BU533405			Db	278	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	337
VERSION	BU533405.1	EST.		Qy	301	TGGGAATTCCAATGAGTATGGCACTAG	327
KEYWORDS	Homo sapiens (human)	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.		Db	338	TGGGAATTCCAATGAGTATGGCACTAG	364
ORGANISM							
REFERENCE	1 (bases 1 to 573)						
AUTHORS	NIH_MGC	http://mgc.nci.nih.gov/					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)						
JOURNAL	Unpublished (1999)						
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgbpbs@nih.gov						
Tissue Procurement	NCI						
CDNA Library Preparation	Michael Brownstein Laboratory						
CDNA Library Arrayed by	The I.M.A.G.E. Consortium (ILNL)						
DNA Sequencing by	Agencourt Bioscience Corporation						
Clone distribution	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:						
Version	1.573						
Source							
Organism	"Homo sapiens"						
/mol type="mRNA"							
/db_xref="txon:9606"							
/clone="IMAGE:6559746"							
/tissue type="mixed (pool of 40 RNAs)"							
/lab_host="DH10B (T1-phage-resistant)"							
/clone lib="NIH_MGC_126"							
/note="Vector: DNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgttcggcc); Double-stranded DNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.1%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:							
	5'-AAGCAGCTGTTGTAACCCAGACTGGCCATTAGGCCGG-3', and 5'-ATTCATGAGGCCAGGGCCACATG-DT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."						
ORIGIN							
Query Match	100.0%	Score 327; DB 3; Length 581;					
Best Local Similarity	100.0%	Pred. No. 6.6e-175;					
Matches	327;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60				
Db	14	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	73				
<b>RESULT 34</b>							
BP308845	BP308845	581 bp mRNA linear EST 17-SEP-2004		Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60
LOCUS	BP308845	Sugano cDNA library, brain Homo sapiens cdNA clone		Db	38	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	97
DEFINITION	NRB06593, mRNA sequence.			Qy	61	CGGTTGAAGTGAAGAAAGTGGATGAGTAGGCCTCTGGCGGGGATATTGGTTGAT	120
ACCESSION	BP308845			Db	98	CGGTTGAAGTGAAGAAACTGGATGAGTAGGCCTCTGGGGATATTGGTTGAT	157
VERSION	BP308845.1	EST.		Qy	121	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	180
KEYWORDS	Homo sapiens (human)			Db	158	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	217
ORGANISM	Homo sapiens			Qy	181	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	240
REFERENCE	1 (bases 1 to 581)			Db	218	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	277
AUTHORS	Suzuki,Y., Yanashita,R., Sakakibara,Y., Chiba,J., Mizushima,Sugano,J., Nakai,K. and Sugano,S.			Qy	241	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	300
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions			Db	278	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	337
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)			Qy	301	TGGGAATTCCAATGAGTATGGCACTAG	327
PUBMED	1542556			Db	338	TGGGAATTCCAATGAGTATGGCACTAG	364
COMMENT	Contact: Yutaka Suzuki Department of Virology, University of Tokyo Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan Email: yszuki@ims.u-tokyo.ac.jp.			Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60
FEATURES	Location/Qualifiers			Db	38	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	97
Source				Qy	61	CGGTTGAAGTGAAGAAAGTGGATGAGTAGGCCTCTGGGGGATATTGGTTGAT	120
Organism	"Homo sapiens"			Db	98	CGGTTGAAGAAACTGGATGAGTAGGCCTCTGGGGATATTGGTTGAT	157
/mol type="mRNA"				Qy	121	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	180
/db_xref="txon:9606"				Db	158	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	217
/clone="IMAGE:6559746"				Qy	181	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	240
/tissue type="brain"				Db	218	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	277
/clone lib="Sugano cDNA library, brain"				Qy	241	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	300
/clone lib="Sugano cDNA library, brain"				Db	278	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	337
ORIGIN				Qy	301	TGGGAATTCCAATGAGTATGGCACTAG	327
Query Match	100.0%	Score 327; DB 3; Length 581;		Db	338	TGGGAATTCCAATGAGTATGGCACTAG	364
Best Local Similarity	100.0%	Pred. No. 6.6e-175;		Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60
Matches	327;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Db	38	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	97
Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60				
Db	14	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	73				
<b>RESULT 35</b>							
BU533405	BU533405	573 bp mRNA linear EST 13-SEP-2002		Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60
LOCUS	AGENCOURT_10197885	NIH_MGC_126 Homo sapiens cDNA clone		Db	38	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	97
DEFINITION	IMAGE:6555746 5'	mRNA sequence.		Qy	61	CGGTTGAAGTGAAGAAAGTGGATGAGTAGGCCTCTGGGGGATATTGGTTGAT	120
ACCESSION	BU533405			Db	98	CGGTTGAAGAAACTGGATGAGTAGGCCTCTGGGGATATTGGTTGAT	157
VERSION	BU533405.1	EST.		Qy	121	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	180
KEYWORDS	Homo sapiens (human)			Db	158	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	217
ORGANISM	Homo sapiens			Qy	181	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	240
REFERENCE	1 (bases 1 to 581)			Db	218	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	277
AUTHORS	Suzuki,Y., Yanashita,R., Sakakibara,Y., Chiba,J., Mizushima,Sugano,J., Nakai,K. and Sugano,S.			Qy	241	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	300
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions			Db	278	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	337
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)			Qy	301	TGGGAATTCCAATGAGTATGGCACTAG	327
PUBMED	1542556			Db	338	TGGGAATTCCAATGAGTATGGCACTAG	364
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan Email: yszuki@ims.u-tokyo.ac.jp.			Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60
FEATURES	Source			Db	38	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	97
Site 1: SfiI (ggccattatggcc); Double-stranded DNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.1%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:				Qy	61	CGGTTGAAGTGAAGAAAGTGGATGAGTAGGCCTCTGGGGGATATTGGTTGAT	120
Site 2: SfiI (ggccgttcggcc);				Db	98	CGGTTGAAGAAACTGGATGAGTAGGCCTCTGGGGGATATTGGTTGAT	157
Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."				Qy	121	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	180
ORIGIN				Db	158	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	217
Query Match	100.0%	Score 327; DB 3; Length 581;		Qy	181	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	240
Best Local Similarity	100.0%	Pred. No. 6.6e-175;		Db	218	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	277
Matches	327;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy	241	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	300
Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60				
Db	14	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	73				
<b>RESULT 36</b>							
BU533405	BU533405	573 bp mRNA linear EST 13-SEP-2002		Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60
LOCUS	AGENCOURT_10197885	NIH_MGC_126 Homo sapiens cDNA clone		Db	38	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	97
DEFINITION	IMAGE:6555746 5'	mRNA sequence.		Qy	61	CGGTTGAAGTGAAGAAAGTGGATGAGTAGGCCTCTGGGGGATATTGGTTGAT	120
ACCESSION	BU533405			Db	98	CGGTTGAAGAAACTGGATGAGTAGGCCTCTGGGGGATATTGGTTGAT	157
VERSION	BU533405.1	EST.		Qy	121	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	180
KEYWORDS	Homo sapiens (human)			Db	158	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	217
ORGANISM	Homo sapiens			Qy	181	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	240
REFERENCE	1 (bases 1 to 581)			Db	218	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	277
AUTHORS	Suzuki,Y., Yanashita,R., Sakakibara,Y., Chiba,J., Mizushima,Sugano,J., Nakai,K. and Sugano,S.			Qy	241	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	300
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions			Db	278	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	337
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)			Qy	301	TGGGAATTCCAATGAGTATGGCACTAG	327
PUBMED	1542556			Db	338	TGGGAATTCCAATGAGTATGGCACTAG	364
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan Email: yszuki@ims.u-tokyo.ac.jp.			Qy	1	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	60
FEATURES	Source			Db	38	ATGGCGCGCAGCTGGATGTCGATGCCCTGGGGGACCAACA GCCTCGGGCGGGCAAGAG	97
Organism	"Homo sapiens"			Qy	61	CGGTTGAAGTGAAGAAAGTGGATGAGTAGGCCTCTGGGGGATATTGGTTGAT	120
/mol type="mRNA"				Db	98	CGGTTGAAGAAACTGGATGAGTAGGCCTCTGGGGGATATTGGTTGAT	157
/db_xref="txon:9606"				Qy	121	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	180
/clone="NRB06593"				Db	158	AACGTGTCATCTGCAGAACCATPATGGATCTTGATGAGATCTCAAGTAACCA	217
/tissue type="brain"				Qy	181	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	240
/clone lib="Sugano cDNA library, brain"				Db	218	GCCTCCGCTACTCTAGAGAGTACTCTGGATGGGAGTGACATGCTTTCAC	277
ORIGIN				Qy	241	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	300
Query Match	100.0%	Score 327; DB 3; Length 581;		Db	278	TTCACATGATCTCTGGCTCAAACAGACAGGAGTGTCATGACACAGGAG	337
Best Local Similarity	100.0%	Pred. No. 6.6e-175;		Qy	301	TGGGAATTCCAATGAGTATGGCACTAG	327
Matches	327;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Db	338	TGGGAATTCCAATGAGTATGGCACTAG	364





Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 801;

Best Local Similarity 100.0%; Pred. No. 6.8e-175; Mismatches 0; Indels 0; Gaps 0;

Matches 327; Conservative 0; Gaps 0;

Db 1 ATGGCGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 60

Db 44 ATGGGGCACGGATGATGGATAACCCAGCGCAACAGGAAAGAG 103

Qy 61 CGCTTGAGTGAAGTAAAAGTGAATCGATGCCCTCTGCCTGGATAATTGTGTGTAT 120

Db 104 CGCTTGAACTGAAAGTGAATCGATGCCCTCTGCCTGGATAATTGTGTGTAT 163

Qy 121 AACGTGCCATCTGAGGAGCACATTATGATGTTGATAGATGTAAGCTAACAG 180

Db 164 AACGTGCCCCATCTGAGAACCATTTGATCATGAAATGTAAGCTAACAG 223

Qy 181 CGCTCGCTACTTCGAAAGTGTACTGGACTCTGAACTATGTTAAC 240

Db 224 GCTGCGCTACTTCGAAAGTGTACTGGACTCTGAACTATGTTAAC 283

Qy 241 TTCCACTGCACTCTCGCTGGCTCAAACACGACAGGTGTCCATTGACAACAGAAG 300

Db 284 TTCCACTGCACTCTCGCTGGCTCAAACACGACAGGTGTCCATTGACAACAGAAG 343

Qy 301 TGGGAAATCCAAGATGGCCACTAG 327

Db 344 TGGGAAATCCAAGATGGCCACTAG 370

RESULT 39  
LOCUS BU959349 845 bp mRNA linear EST 21-OCT-2002  
DEFINITION AGNCOURT\_10622637 NIH\_MGC\_127 Homo sapiens cDNA clone IMAGE:6737564 5', mRNA sequence.

ACCESSION BU959349  
VERSION 1 GI:2418921  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
1 (bases 1 to 845)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgbps-r@mail.nih.gov  
Tissue Procurement: NCI  
cDNA Library Preparation: Michael Brownstein Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
http://image.llnl.gov  
Plate: LICM3067 row: m column: 19  
High quality sequence stop: 424.  
Location/Qualifiers

1..845  
/organism="Homo sapiens"  
/mol\_type="mRNA"

/db\_xref="taxon:9606"  
/clone="IMAGE:6737564"

/tissue\_type="mixed (pool of 40 RNAs)"

/lab\_host="DH10B (T1-phage-resistant)"

/clone\_id="NIH\_MGC\_127"

/note="Vector: PDMR-LIB; Site\_1: SfII (ggccattatggcc);

Site\_2: SII (ggccggctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder

- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%. 5, and 3, adaptors were used in cloning as follows: 5'-AAGGAGTGTATCAACGAGAGNGCCATTACGCCGG-3' and 5'-ATTCATAGGCCGGCCGGAGATG-DT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH MGC 126 and NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 845;  
Best Local Similarity 100.0%; Pred. No. 6.8e-175; Mismatches 0; Indels 0; Gaps 0;  
Matches 327; Conservative 0; Gaps 0;

1 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 60  
22 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 81  
61 CGCTTGAGTGAAGAAAAGTGAATGTCAGTAGCCCTCTGGCCCTGGATATGGTTGAT 120  
82 CGCTTGAGTGAAGTGAAGATGGCTAGAGATGTCAGCTGGATTTGTGTGTAT 141  
121 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 180  
142 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 201  
181 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 240  
202 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 261  
Qy 1 Db 1  
Qy 2 Db 2  
Qy 3 Db 3  
Qy 4 Db 4  
Qy 5 Db 5  
Qy 6 Db 6  
Qy 7 Db 7  
Qy 8 Db 8  
Qy 9 Db 9  
Qy 10 Db 10  
Qy 11 Db 11  
Qy 12 Db 12  
Qy 13 Db 13  
Qy 14 Db 14  
Qy 15 Db 15  
Qy 16 Db 16  
Qy 17 Db 17  
Qy 18 Db 18  
Qy 19 Db 19  
Qy 20 Db 20  
Qy 21 Db 21  
Qy 22 Db 22  
Qy 23 Db 23  
Qy 24 Db 24  
Qy 25 Db 25  
Qy 26 Db 26  
Qy 27 Db 27  
Qy 28 Db 28  
Qy 29 Db 29  
Qy 30 Db 30  
Qy 31 Db 31  
Qy 32 Db 32  
Qy 33 Db 33  
Qy 34 Db 34  
Qy 35 Db 35  
Qy 36 Db 36  
Qy 37 Db 37  
Qy 38 Db 38  
Qy 39 Db 39  
Qy 40 Db 40

Query Match 100.0%; Score 327; DB 5; Length 845;  
Best Local Similarity 100.0%; Pred. No. 6.8e-175; Mismatches 0; Indels 0; Gaps 0;  
Matches 327; Conservative 0; Gaps 0;

1 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 60  
22 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 81  
61 CGCTTGAGTGAAGAAAAGTGAATGTCAGTAGCCCTCTGGCCCTGGATATGGTTGAT 120  
82 CGCTTGAGTGAAGTGAAGATGGCTAGAGATGTCAGCTGGATTTGTGTGTAT 141  
121 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 180  
142 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 201  
181 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 240  
202 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 261  
Qy 1 Db 1  
Qy 2 Db 2  
Qy 3 Db 3  
Qy 4 Db 4  
Qy 5 Db 5  
Qy 6 Db 6  
Qy 7 Db 7  
Qy 8 Db 8  
Qy 9 Db 9  
Qy 10 Db 10  
Qy 11 Db 11  
Qy 12 Db 12  
Qy 13 Db 13  
Qy 14 Db 14  
Qy 15 Db 15  
Qy 16 Db 16  
Qy 17 Db 17  
Qy 18 Db 18  
Qy 19 Db 19  
Qy 20 Db 20  
Qy 21 Db 21  
Qy 22 Db 22  
Qy 23 Db 23  
Qy 24 Db 24  
Qy 25 Db 25  
Qy 26 Db 26  
Qy 27 Db 27  
Qy 28 Db 28  
Qy 29 Db 29  
Qy 30 Db 30  
Qy 31 Db 31  
Qy 32 Db 32  
Qy 33 Db 33  
Qy 34 Db 34  
Qy 35 Db 35  
Qy 36 Db 36  
Qy 37 Db 37  
Qy 38 Db 38  
Qy 39 Db 39  
Qy 40 Db 40

Query Match 100.0%; Score 327; DB 5; Length 845;  
Best Local Similarity 100.0%; Pred. No. 6.8e-175; Mismatches 0; Indels 0; Gaps 0;  
Matches 327; Conservative 0; Gaps 0;

1 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 60  
22 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 81  
61 CGCTTGAGTGAAGAAAAGTGAATGTCAGTAGCCCTCTGGCCCTGGATATGGTTGAT 120  
82 CGCTTGAGTGAAGTGAAGATGGCTAGAGATGTCAGCTGGATTTGTGTGTAT 141  
121 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 180  
142 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 201  
181 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 240  
202 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 261  
Qy 1 Db 1  
Qy 2 Db 2  
Qy 3 Db 3  
Qy 4 Db 4  
Qy 5 Db 5  
Qy 6 Db 6  
Qy 7 Db 7  
Qy 8 Db 8  
Qy 9 Db 9  
Qy 10 Db 10  
Qy 11 Db 11  
Qy 12 Db 12  
Qy 13 Db 13  
Qy 14 Db 14  
Qy 15 Db 15  
Qy 16 Db 16  
Qy 17 Db 17  
Qy 18 Db 18  
Qy 19 Db 19  
Qy 20 Db 20  
Qy 21 Db 21  
Qy 22 Db 22  
Qy 23 Db 23  
Qy 24 Db 24  
Qy 25 Db 25  
Qy 26 Db 26  
Qy 27 Db 27  
Qy 28 Db 28  
Qy 29 Db 29  
Qy 30 Db 30  
Qy 31 Db 31  
Qy 32 Db 32  
Qy 33 Db 33  
Qy 34 Db 34  
Qy 35 Db 35  
Qy 36 Db 36  
Qy 37 Db 37  
Qy 38 Db 38  
Qy 39 Db 39  
Qy 40 Db 40

Query Match 100.0%; Score 327; DB 5; Length 845;  
Best Local Similarity 100.0%; Pred. No. 6.8e-175; Mismatches 0; Indels 0; Gaps 0;  
Matches 327; Conservative 0; Gaps 0;

1 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 60  
22 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 81  
61 CGCTTGAGTGAAGAAAAGTGAATGTCAGTAGCCCTCTGGCCCTGGATATGGTTGAT 120  
82 CGCTTGAGTGAAGTGAAGATGGCTAGAGATGTCAGCTGGATTTGTGTGTAT 141  
121 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 180  
142 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 201  
181 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 240  
202 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 261  
Qy 1 Db 1  
Qy 2 Db 2  
Qy 3 Db 3  
Qy 4 Db 4  
Qy 5 Db 5  
Qy 6 Db 6  
Qy 7 Db 7  
Qy 8 Db 8  
Qy 9 Db 9  
Qy 10 Db 10  
Qy 11 Db 11  
Qy 12 Db 12  
Qy 13 Db 13  
Qy 14 Db 14  
Qy 15 Db 15  
Qy 16 Db 16  
Qy 17 Db 17  
Qy 18 Db 18  
Qy 19 Db 19  
Qy 20 Db 20  
Qy 21 Db 21  
Qy 22 Db 22  
Qy 23 Db 23  
Qy 24 Db 24  
Qy 25 Db 25  
Qy 26 Db 26  
Qy 27 Db 27  
Qy 28 Db 28  
Qy 29 Db 29  
Qy 30 Db 30  
Qy 31 Db 31  
Qy 32 Db 32  
Qy 33 Db 33  
Qy 34 Db 34  
Qy 35 Db 35  
Qy 36 Db 36  
Qy 37 Db 37  
Qy 38 Db 38  
Qy 39 Db 39  
Qy 40 Db 40

REFERENCE /organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6737564"

/tissue\_type="mixed (pool of 40 RNAs)"

/lab\_host="DH10B (T1-phage-resistant)"

/clone\_id="NIH\_MGC\_127"

/note="Vector: PDMR-LIB; Site\_1: SfII (ggccattatggcc);

Site\_2: SII (ggccggctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder

Query Match 100.0%; Score 327; DB 5; Length 845;  
Best Local Similarity 100.0%; Pred. No. 6.8e-175; Mismatches 0; Indels 0; Gaps 0;  
Matches 327; Conservative 0; Gaps 0;

1 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 60  
22 ATGGGGCAGGATGATGGATAACCCAGCGCAACAGGAAAGAG 81  
61 CGCTTGAGTGAAGAAAAGTGAATGTCAGTAGCCCTCTGGCCCTGGATATGGTTGAT 120  
82 CGCTTGAGTGAAGTGAAGATGGCTAGAGATGTCAGCTGGATTTGTGTGTAT 141  
121 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 180  
142 AACGTGCCATCTCGAGGACCAATTGGATCTTGCATGAACTGGTAACGAAAC 201  
181 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 240  
202 GCGTCCGCTACTCTGAGAAGTGTACTGGACTCTGAACTATGTTTCAC 261  
Qy 1 Db 1  
Qy 2 Db 2  
Qy 3 Db 3  
Qy 4 Db 4  
Qy 5 Db 5  
Qy 6 Db 6  
Qy 7 Db 7  
Qy 8 Db 8  
Qy 9 Db 9  
Qy 10 Db 10  
Qy 11 Db 11  
Qy 12 Db 12  
Qy 13 Db 13  
Qy 14 Db 14  
Qy 15 Db 15  
Qy 16 Db 16  
Qy 17 Db 17  
Qy 18 Db 18  
Qy 19 Db 19  
Qy 20 Db 20  
Qy 21 Db 21  
Qy 22 Db 22  
Qy 23 Db 23  
Qy 24 Db 24  
Qy 25 Db 25  
Qy 26 Db 26  
Qy 27 Db 27  
Qy 28 Db 28  
Qy 29 Db 29  
Qy 30 Db 30  
Qy 31 Db 31  
Qy 32 Db 32  
Qy 33 Db 33  
Qy 34 Db 34  
Qy 35 Db 35  
Qy 36 Db 36  
Qy 37 Db 37  
Qy 38 Db 38  
Qy 39 Db 39  
Qy 40 Db 40

REFERENCE /organism="Homo sapiens"

AUTHORS

TITLE

JOURNAL

COMMENT

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LICM1435; row: p; column: 13

High quality sequence stop: 529.



FEATURES	source	FEATURES	source	Location/Qualifiers
		High quality sequence stop: 543.		
Location/Qualifiers		1. .1098		/organism="Homo sapiens"
/organism="Homo sapiens"		2. .945		/mol_type="mRNA"
/mol_type="mRNA"		3. .966		/db_xref="TAXON:9606"
/db_xref="TAXON:9606"		4. .96		/clone="IMAGE:6049202"
/clone="IMAGE:6049202"		5. .96		/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"		6. .96		/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"		7. .96		/clone_id="NIH_MGC_71"
/clone_id="NIH_MGC_71"		8. .96		/note="Organ: uterine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 2 kb."
		9. .96		Average insert size 2 kb. Library constructed by Life Technologies."
ORIGIN				
Query Match		Score 327; DB 3; Length 945;		Score 327; DB 3; Length 1098;
Best Local Similarity 100.0%		Score 327; DB 3; Length 945;		Score 327; DB 3; Length 1098;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Score 327; DB 3; Length 945;		Score 327; DB 3; Length 1098;
Qy 1 ATGGCGCAAGCATTGATGTGGATAACCCGACGGCACAACAGCGCCGGCAAGAG 60	Qy	1 ATGGCGCAAGCATTGATGTGGATAACCCGACGGCACAACAGCGCCGGCAAGAG 60	Qy	1 ATGGCGCAAGCATTGATGTGGATAACCCGACGGCACAACAGCGCCGGCAAGAG 60
Db 33 ATGGCGCAAGCATTGATGTGGATAACCCGACGGCACAACAGCGCCGGCAAGAG 92	Db	33 ATGGCGCAAGCATTGATGTGGATAACCCGACGGCACAACAGCGCCGGCAAGAG 92	Db	33 ATGGCGCAAGCATTGATGTGGATAACCCGACGGCACAACAGCGCCGGCAAGAG 92
Qy 61 CGCTTGAAGTGAAGTGGAAAGTGGATAGCAGTAGGCCCTCGGCTGGATATGGTTGAT 120	Qy	61 CGCTTGAAGTGAAGTGGAAAGTGGATAGCAGTAGGCCCTCGGCTGGATATGGTTGAT 120	Qy	61 CGCTTGAAGTGAAGTGGAAAGTGGATAGCAGTAGGCCCTCGGCTGGATATGGTTGAT 120
Db 93 CGCTTGAAGTGAAGTGAAGTGGAAAGTGGATAGCAGTAGGCCCTCGGCTGGATATGGTTGAT 152	Db	93 CGCTTGAAGTGAAGTGAAGTGGAAAGTGGATAGCAGTAGGCCCTCGGCTGGATATGGTTGAT 152	Db	93 CGCTTGAAGTGAAGTGGAAAGTGGATAGCAGTAGGCCCTCGGCTGGATATGGTTGAT 152
Qy 121 AACTGTCCATCTGCAGAACACATTAATGGATCTTGATAGAATGTCAGCTAACAG 180	Qy	121 AACTGTCCATCTGCAGAACACATTAATGGATCTTGATAGAATGTCAGCTAACAG 180	Qy	121 AACTGTCCATCTGCAGAACACATTAATGGATCTTGATAGAATGTCAGCTAACAG 180
Db 153 AACTGTCCATCTGCAGAACACATTAATGGATCTTGATAGAATGTCAGCTAACAG 212	Db	153 AACTGTCCATCTGCAGAACACATTAATGGATCTTGATAGAATGTCAGCTAACAG 212	Db	153 AACTGTCCATCTGCAGAACACATTAATGGATCTTGATAGAATGTCAGCTAACAG 212
Qy 181 GGTGCCCCTACTCTAGAGAGTGTACTGTGATGGGGAGTGTACATGCTTTTCAC 240	Qy	181 GGTGCCCCTACTCTAGAGAGTGTACTGTGATGGGGAGTGTACATGCTTTTCAC 240	Qy	181 GGTGCCCCTACTCTAGAGAGTGTACTGTGATGGGGAGTGTACATGCTTTTCAC 240
Db 213 GCGTCCGCTACTCTAGAGAGTGTACTGTGATGGGGAGTGTACATGCTTTTCAC 272	Db	213 GCGTCCGCTACTCTAGAGAGTGTACTGTGATGGGGAGTGTACATGCTTTTCAC 272	Db	213 GCGTCCGCTACTCTAGAGAGTGTACTGTGATGGGGAGTGTACATGCTTTTCAC 272
Qy 241 TTCCACTGCATCTCGCTGGCTCAAACACAGCACAGGTGTGTCATMGCACAGAG 300	Qy	241 TTCCACTGCATCTCGCTGGCTCAAACACAGCACAGGTGTGTCATMGCACAGAG 300	Qy	241 TTCCACTGCATCTCGCTGGCTCAAACACAGCACAGGTGTGTCATMGCACAGAG 300
Db 273 TTCCACTGCATCTCGCTGGCTCAAACACAGCACAGGTGTGTCATMGCACAGAG 332	Db	273 TTCCACTGCATCTCGCTGGCTCAAACACAGCACAGGTGTGTCATMGCACAGAG 332	Db	273 TTCCACTGCATCTCGCTGGCTCAAACACAGCACAGGTGTGTCATMGCACAGAG 332
Qy 301 TGGGAATTCCAAGTATGGGACTAG 327	Qy	301 TGGGAATTCCAAGTATGGGACTAG 327	Qy	301 TGGGAATTCCAAGTATGGGACTAG 327
Db 333 TGGGAATTCCAAGTATGGGACTAG 359	Db	333 TGGGAATTCCAAGTATGGGACTAG 359	Db	333 TGGGAATTCCAAGTATGGGACTAG 359
RESULT 43				Search completed: March 15, 2006, 11:25:40
BQ050461		BQ050461 1098 bp mRNA linear EST 29-MAR-2002		Job time : 3739 secs
DEFINITION		AGENCOURT 7050949 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5784423		
ACCESSION		5' mRNA Sequence.		
VERSION		1 (bases 1 to 1098).		
KEYWORDS		National Institutes of Health Mammalian Gene Collection (MGC)		
SOURCE		Unpublished (1999)		
ORGANISM		Contact: Robert Strainsberg, Ph.D.		
		Email: cgbps-r@mail.nih.gov		
REFERENCE		Tissue Procurement: ATCC		
AUTHORS		CDNA Library Preparation: Life Technologies, Inc.		
TITLE		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (L1NL)		
JOURNAL		DNA Sequencing by: Agencourt Bioscience Corporation		
COMMENT		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/L1NL at:		
		<a href="http://image.lnl.gov">http://image.lnl.gov</a>		
		High quality sequence stop: 548.		
		Row: 0		
		Column: 16		

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 12:22:08 ; Search time 368.547 Seconds  
(without alignments)  
5913.368 Million cell updates/sec

Title: US-09-541-462B-1  
Perfect score: 327  
Sequence: 1 atgcggcagcgatggatgt.....tccaaaatggcactag 327

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 12

Total number of hits satisfying chosen parameters: 116703

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_21:  
 1: geneseqn1980s:  
 2: geneseqn1990s:  
 3: geneseqn2000s:  
 4: geneseqn2001as:  
 5: geneseqn2001bs:  
 6: geneseqn2002as:  
 7: geneseqn2002bs:  
 8: geneseqn2003as:  
 9: geneseqn2003bs:  
 10: geneseqn2003s:  
 11: geneseqn2003ab:  
 12: geneseqn2004ab:  
 13: geneseqn2004bs:  
 14: geneseqn2005s:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	327	100.0	327	3	AAA96882	Aaa96882 Nucleotid
2	327	100.0	482	3	AAC03896	Aac03896 Human sec
3	327	100.0	506	12	AD087496	Ad087496 Human tum
4	327	100.0	506	12	AD087156	Ad087156 Human tum
5	327	100.0	506	12	ADQ4881	Adq4881 Human tum
6	327	100.0	508	3	AAA74978	Aaa74978 DNA encod
7	327	100.0	508	13	ACN40951	Ach40951 Tumour-as
8	325	99.4	476	9	ACH29979	Ach29979 Human tes
c 9	321	98.2	3726	13	AD05913	Ad05913 Human the
c 10	321	98.2	4543	11	ACN90161	Acn90161 Breast ca
c 11	320	97.9	503	12	ADQ9179	Adq9179 Human pro
c 12	308	94.2	4476	5	ABV25615	Abv25615 Human pro
c 13	296	90.5	311	14	ACI57420	aci57420 Human col
c 14	296	90.5	3484	12	ADF42703	Adf42703 Human Tes
c 15	296	90.5	3484	12	ADQ18564	Adq18564 Human sof
c 16	296	90.5	3484	13	ADQ89865	Adq89865 Human SPA
c 17	296	90.5	511	10	ADB7558	Adb7558 Prostate
c 18	296	90.5	5371	12	ADD23032	Add23032 Human sof
c 19	267	81.7	5347	6	AAS94844	Aas94844 Human DNA

## ALIGNMENTS

RESULT 1	
ID	AAA66882 standard; DNA; 327 BP.
XX	
AC	AAA96882;
XX	
DT	19-FEB-2001 (first entry)
XX	
DE	Nucleotide sequence of human ring finger protein ROC1.
XX	
KW	ROC1; Roc2; cullin; ring finger protein; APC complex; SCF pathway;
KW	Cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation; tumour; ss.
XX	
OS	Homo sapiens.
XX	
FH	Location/Qualifiers
PT	1..327
FT	/tag= a
FT	/product= "ROC1"
XX	
PN	WO200058472-A2.
XX	
PD	05-OCT-2000.
PF	31-MAR-2000; 20000WO-US008592.
XX	
PR	31-MAR-1999; 99US-0127261P.
PR	22-NOV-1999; 99US-0166927P.
XX	
PA	(UNNC-) UNIV NORTH CAROLINA.
XX	
PI	Xiong Y, Ohta T;
XX	
DR	WPI; 2000-647235/62.
DR	P-PSDB; AAB19160.
XX	
PT	Novel nucleic acid encoding cullin regulating ring finger proteins, termed as ROC proteins similar to anaphase-promoting complex 11, for therapeutic and diagnostic use.
XX	
PS	Claim 1; Fig 2A; 83pp; English.





cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAR sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAR cDNA sequence from the present invention.

XX Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Query Match 100.0%; Score 327; DB 12; Length 506;  
Best Local Similarity 100.0%; Pred. No. 2.6e-15;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGCAGCGATTGATGTGGTACCCGGAGCGCAACACGGGCCAACAGAG 60  
DB 6 ATGGGGCAGCGATTGATGTGGTACCCGGAGCGCAACACGGGCCAACAGAG 65  
QY 61 CGCTTTGAATGTGAAATGGAAATGCAAGTAGCCTCTGGCCCTGGATAATTGGTGTAT 120  
DB 66 CGCTTTGAATGTGAAATGGAAATGCAAGTAGCCTCTGGCCCTGGATAATTGGTGTAT 125  
QY 121 AACCTGTGCCATCTTGACATATTGGATCTTGCATAGATGTCAAGCTAACAG 180  
DB 126 AACCTGTGCCATCTTGACACCATTTGGATCTTGCATAGATGTCAACACAG 185  
QY 181 GCGTGGCGTACTCTGAAAGTGTACTCTGCGGAGCTGATGGTACCTTCAC 240  
DB 186 GCGTGGCGTACTCTGAAAGTGTACTCTGCGGAGCTGATGGTACCTTCAC 245  
QY 241 TTCCACTGTGATCTCTGGCTGCTCAAACAGCAAGGTGTCCATTGGACACAGAG 300  
DB 246 TTCCACTGTGATCTCTGGCTGCTCAAACAGCAAGGTGTCCATTGGACACAGAG 305  
QY 301 TGGGAATTCCAAAAGTATGGCACTAG 327  
DB 306 TGGGAATTCCAAAAGTATGGCACTAG 332

**RESULT 5**  
ADQ84881 standard; cDNA; 506 BP.  
XX ADQ84881; Score 327; DB 13; Length 506;  
AC 100.0%; Pred. No. 2.6e-15;  
DT 07-OCT-2004 (first entry)  
XX Human tumour-associated antigenic target (TAT) cDNA sequence #1695.  
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
KW cancer; cell proliferative disorder; gene; ss.  
OS Homo sapiens.  
PN WO200406270-A2.  
XX 22-JUL-2004.  
XX 15-OCT-2003; 2003WO-US029126.  
XX 18-OCT-2002; 2002US-0418988P.  
PA (GEFH) GENENTECH INC.  
PA (WUDI) WU T D.  
PA (ZHOU) ZHOU Y.  
XX 241 TTCCACTGTGATCTCTGGCTGCTCAAACAGCAAGGTGTACTCTGGACAG 300  
XX 246 TTCCACTGTGATCTCTGGCTGCTCAAACAGCAAGGTGTACTCTGGACAG 305

XX	WPI; 2004-534300/51.	DR			
XX	New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.	PT			
XX	Claim 1; SEQ ID NO 1695; 5504pp; English.	PT			
XX	The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO: 1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon growth potential; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.	CC			
XX	Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;	SQ			
XX	Query Match 100.0%; Score 327; DB 13; Length 506; Best Local Similarity 100.0%; Pred. No. 2.6e-15; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	1 ATGGGGCAGCGATTGATGTGGTACCCGGAGCGCAACACGGGCCAACAGAG 60 DB 6 ATGGGGCAGCGATTGATGTGGTACCCGGAGCGCAACACGGGCCAACAGAG 65 QY 61 CGCTTTGAATGTGAAATGGAAATGCAAGTAGCCTCTGGCCCTGGATAATTGGTGTAT 120 DB 66 CGCTTTGAATGTGAAATGGAAATGCAAGTAGCCTCTGGCCCTGGATAATTGGTGTAT 125 QY 121 AACCTGTGCCATCTTGACATATTGGATCTTGCATAGATGTCAAGCTAACAG 180 DB 126 AACCTGTGCCATCTTGACACCATTTGGATCTTGCATAGATGTCAACACAG 185 QY 181 GCGTGGCGTACTCTGAAAGTGTACTCTGGAGGAGCTGATGGTACCTTCAC 240 DB 186 GCGTGGCGTACTCTGAAAGTGTACTCTGGAGGAGCTGATGGTACCTTCAC 245 QY 241 TTCCACTGTGATCTCTGGCTGCTCAAACAGCAAGGTGTCCATTGGACACAGAG 300 DB 246 TTCCACTGTGATCTCTGGCTGCTCAAACAGCAAGGTGTCCATTGGACACAGAG 305 QY 301 TGGGAATTCCAAAAGTATGGCACTAG 327 DB 306 TGGGAATTCCAAAAGTATGGCACTAG 332	DB	
XX	Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;	SQ			
XX	Query Match 100.0%; Score 327; DB 13; Length 506; Best Local Similarity 100.0%; Pred. No. 2.6e-15; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	1 ATGGGGCAGCGATTGATGTGGTACCCGGAGCGCAACACGGGCCAACAGAG 60 DB 6 ATGGGGCAGCGATTGATGTGGTACCCGGAGCGCAACACGGGCCAACAGAG 65 QY 61 CGCTTTGAATGTGAAATGGAAATGCAAGTAGCCTCTGGCCCTGGATAATTGGTGTAT 120 DB 66 CGCTTTGAATGTGAAATGGAAATGCAAGTAGCCTCTGGCCCTGGATAATTGGTGTAT 125 QY 121 AACCTGTGCCATCTTGACATATTGGATCTTGCATAGATGTCAAGCTAACAG 180 DB 126 AACCTGTGCCATCTTGACACCATTTGGATCTTGCATAGATGTCAACACAG 185 QY 181 GCGTGGCGTACTCTGAAAGTGTACTCTGGAGGAGCTGATGGTACCTTCAC 240 DB 186 GCGTGGCGTACTCTGAAAGTGTACTCTGGAGGAGCTGATGGTACCTTCAC 245 QY 241 TTCCACTGTGATCTCTGGCTGCTCAAACAGCAAGGTGTCCATTGGACACAGAG 300 DB 246 TTCCACTGTGATCTCTGGCTGCTCAAACAGCAAGGTGTCCATTGGACACAGAG 305	DB	

Qy	301	TGGGAATTCAAAGTATGGCACTAG	327
Db	306	TGGGAATTCAAAGTATGGCACTAG	332
RESULT 6			
AAA74978			
ID		AAA74978 standard; DNA;	508 BP.
XX			
AC			
XX			
DT	02-JAN-2001	(first entry)	
XX		DNA encoding a human cullin-interacting RING-H2 finger protein (Rbx1).	
DE			
XX		Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;	
RW		tumour suppressor; carcinoma; Ring box association; carcinoma;	
RW		von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;	
RW		cerebellar hemangioblastoma; hemangioma; retinal angioma;	
RW		pheochromocytomas; <sup>88</sup> .	
OS		Homo sapiens.	
XX			
Key		Location/Qualifiers	
PN	FH	7 . .333	
FT		/*tag= a	
FT		/product= "cullin-interacting RING-H2 finger protein	
FT		(Rbx1)"	
FT			
XX			
W0200050445-A1.			
XX		31-AUG-2000.	
PD		25-FEB-2000; 2000WO-US004838.	
XX		26-FEB-1999; 99US-0121787P.	
PR		(OKLA-) OKLAHOMA MEDICAL RES FOUND.	
PA		XX	
PI		Conaway JA, Conaway RC, Kamura T;	
XX		DR; 2000-522067/53.	
DR		DR-PSDB; AAB08813.	
XX			
PT		Cullin interacting RING-H2 finger protein, a component of von Hippel-Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF) ubiquitin ligase, useful for diagnosing and treating Ring box protein associated carcinomas.	
PT			
PT		XX	
PT		The present sequence encodes a human cullin-interacting RING-H2 finger protein (Ring box protein), designated Rbx1. The polypeptide is a tumour suppressor. Rbx1 is useful for diagnosing a predisposition of a patient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas or augmenting metabolically deficient system in animals. Rbx1 is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Rbx1 can be used to screen for agents which augment or inhibit the activity of other cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau) complex controlling the conjugation of ubiquitin or ubiquitin-like proteins to various sets of target proteins. Carcinomas which may be treated include renal carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal angiomas and pheochromocytomas	
PS		XX	
PS		Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;	
SQ			
Query Match		Score 327; DB 3; Length 508;	
Best Local Similarity		Pred. No. 2.6e-157;	
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
1 ATGGGGGAGGGGATGGGATACCCGAGCGACCAACAGGGGGAAAGAG 60			

molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention.

Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;

Query Match 100.0%; Score 327; DB 13; Length 508;  
Best Local Similarity 100.0%; Pred. No. 2 6e-157;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGTGTGGATACCCGAGGGCACCAACAGGCCGCGGGCAAGAAG 60  
Db 7 ATGGGGCAGCGTGTGGATACCCGAGGGCACCAACAGGCCGCGGGCAAGAAG 66

QY 61 CGCTTTGAACTGTGAAAGGNGGAATGGCAGTAGCCCTCTGGCCMTCGGPATTGNGTGTAT 120  
Db 67 CGCTTTGAACTGTGAAAGGNGGAATGGCAGTAGCCCTCTGGCCMTCGGPATTGNGTGTAT 126

QY 121 AACPTGCCCCATCTGAGGACCACTTGTGATAGATGTAAGGTAAACCAAG 180  
Db 127 AACCTGTGCCATCTGAGGACCACTTGTGATAGATGTAAGGTAAACCAAG 186

QY 181 GCGTCCGGCTACTTCGAGAAGTGTACTGTCGATGGGAGTCGTAACCATGCTTTCAC 240  
Db 187 GCGTCCGGCTACTTCGAGAAGTGTACTGTCGATGGGAGTCGTAACCATGCTTTCAC 246

QY 241 TTCCCACTGATCTCTGCTGGCTCAAACAGGAAAGGTGTCCATTGGCAACAGAG 300  
Db 247 TTCCCACTGATCTCTGCTGGCTCAAACAGGAAAGGTGTCCATTGGCAACAGAG 306

QY 301 TGGGAATTCAAAAGTATGGCACTAG 327  
Db 307 TGGGAATTCAAAAGTATGGCACTAG 333

RESULT 8  
ACH29979 standard; cDNA; 476 BP.

XX AC ACH29979;  
XX DT 13-OCT-2003 (first entry)

XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;

XX KW genome mapping; biodiversity; genetic disorder.

XX Homo sapiens.

XX US2003073623-A1.

XX 17-APR-2003.  
XX PD 30-JUL-2001; 2001US-00918995.

XX PR 30-JUL-2001; 2001US-00918995.

XX PA (DRMANAC R T.  
(LABA/ LABAT I.  
(STAC/ STACHE-CRAIN B.  
(DICK/ DICKSON M. C.  
(JONE/ JONES L W.

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX WP; 2003-615964/58.

PT New polynucleotide sequences obtained from various cDNA libraries, useful PT as hybridization probes, as oligomers for PCR, for chromosome and gene PT mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

XX Claim 1; SEQ ID NO 17191; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of CC 38043 cDNA sequences, appearing as ACH12789-Ach50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also CC included is a purified polypeptide comprising a sequence corresponding to CC a reading frame of the novel polynucleotide. The nucleic acid sequences CC are useful in diagnostics as expressed sequence tags (EST) for CC identifying expressed genes or for physical mapping of the human genome, CC in forensics, in assessing biodiversities, or in identifying mutations CC responsible for genetic disorders and other traits. The nucleotide CC sequences are also useful as hybridisation probes, as oligomers for PCR, CC for chromosome and gene mapping, in the recombinant production of CC protein, or in generating antisense DNA or RNA. The purified polypeptide CC is useful for generating antibodies specific for it. The present sequence CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data CC for this patent did not form part of the printed specification, but was CC obtained in electronic format directly from USPTO at CC sedata.uspto.gov/sequence.html?DocID=2003073623

XX SQ Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;  
XX Query Match 99.4%; Score 325; DB 9; Length 476;  
Best Local Similarity 100.0%; Pred. No. 2.7e-156;  
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCGCAGGATGGATGTCGATACCCGAGGGCACCAAGCGCGCGGGCAAGAAGCC 62  
Db 74 GGCGCAGGATGGATGTCGATACCCGAGGGCACCAAGCGCGCGGGCAAGAAGCC 133  
QY 63 CTTTGAAGTGAAGAAGTGGAAATGGAGTAGCCCTGGGCTGGATAATGGTTGATAA 122  
Db 134 CTTTGAAGTGAAGAAGTGGAAATGGAGTAGCCCTGGGCTGGATAATGGTTGATAA 193  
QY 123 CTGTCGCATCTGCGAGAACACATTATGGATCATGTAATGTCAGCTAACAGGGC 182  
Db 194 CTGTCGCATCTGCGAGAACACATTATGGATCATGTAATGTCAGCTAACAGGGC 253  
QY 183 GTCCGCTACTTCGAGAGTGTACTGTCGATCGGGAGSTGTCGATCATGGCTTCACCT 242  
Db 254 GTCCGCTACTTCGAGAGTGTACTGTCGATCATGGCTTCACCT 313  
QY 303 GGAACTCAAAGATGGGACTAG 327  
Db 374 GGAACTCAAAGATGGGACTAG 398

RESULT 9  
ADS09913/C  
ID ADS09913 standard; DNA; 3726 BP.  
XX AC ADS09913;  
XX DT 16-DEC-2004 (first entry)  
XX Human therapeutic DNA - SEQ ID 150.  
DE Human  
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
KW inflammatory; haemopoiesis; immunity; neurodegenerative; stem cell;  
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

XX DT 02-DEC-2004 (first entry)  
 OS XX Breast cancer related marker, seq id 11311.  
 PN XX DE  
 XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.  
 XX KW  
 XX 23-SEP-2004.  
 PD XX  
 XX Homo sapiens.  
 PF XX  
 XX OS  
 XX PN US2003099974-A1.  
 PR XX  
 XX PD 29-MAY-2003.  
 XX XX  
 PA XX PP 18-JUL-2002; 2002US-00198846.  
 XX (NUVE-) NUVELO INC.  
 XX DR 18-JUL-2001; 2001US-0306220P.  
 XX WPI; 2004 668857/65.  
 DR XX PA (MILL-) MILLENNIUM PHARM INC.  
 XX PI Lillie J, Xu Y, Wang Y, Steinmann K;  
 XX PR 2003-787014/74.  
 PT Novel isolated polypeptide associated with breast cancer, useful for  
 detecting presence of polypeptide in sample, as a marker for breast  
 cancer.  
 PS XX Disclosure: SEQ ID NO 11311; 36PD; English.  
 CC XX The invention relates to an isolated polypeptide (I) associated with  
 CC breast cancer which is encoded by a nucleic acid molecule comprising a  
 CC nucleotide sequence (S1). Further disclosed is an antibody that binds to  
 CC the polypeptide of the invention. The activity of the polypeptide of the  
 CC invention may be described as cytostatic. The antibody is useful for  
 CC detecting the presence of (I) in a sample. Nucleic acid molecules of the  
 CC invention are useful in the detection of breast tumors. (I) is useful as  
 CC a marker for breast cancer and in breast cancer therapy. Sequences Given  
 CC in records ACN78851-ACN92934 represent nucleic acid markers associated  
 CC with breast cancer. Note: The sequence listing does not form part of the  
 CC specification but may be obtained in electronic format from the USPTO web  
 site at seqdata.uspto.gov/sequence.html?DocID=2003009974  
 CC  
 XX SQ Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;  
 CC  
 XX SQ Query Match Similarity 100.0%; Pred. No. 2.9e-154; Score 321; DB 11; Length 4543;  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Sequence 4543 BP; 1069 A; 1171 C; 1083 G; 1220 T; 0 U; 0 Other;  
 CC  
 XX SQ Query 7 GCAGCGATGGATGTTGATTAACCCGAGCAGGGACCAACAGGCCTGGCTGGATATTGTGTTGATACTGT 66  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 67 GAAGTGAAGAAGTGGAAATGGAGTAGCCCTCTGGCTGGATATTGTGTTGATACTGT 126  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 492 GCAGCGATGGATGTTGATTAACCCGAGCAGGGACCAACAGGCCTGGCTGGATATTGTGTTGATACTGT 433  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 432 GAAGTGAAGAAGTGGAAATGGAGTAGCCCTCTGGCTGGATATTGTGTTGATACTGT 373  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 127 GCCATCTGAGGAAACACATTATGGATTCAGTAAGAATGTCAGTAACTTGATAGATGCTTCACTTCAC 186  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 372 GGCATCTGAGGAAACACATTATGGATTCAGTAAGTCACTTCAC 313  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 187 GCTACTTCAAGAAGTGTACTGTGCTGGAACTCTGTAACCATGCTTCACTTCAC 246  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 312 GCTACTTCAAGAAGTGTACTGTGCTGGAACTCTGTAACCATGCTTCACTTCAC 253  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 67 GAACTGAAAGAAGTGGAAATGGAGTAGCTGGCTGGATATTGTGTTGATACTGT 126  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 965 GCCATCTGAGGAAACACATTATGGATTCAGTAAGTCACTTCAC 186  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 1025 GAAGTGAAGAAGTGGAAATGGAGTAGCTGGCTGGATATTGTGTTGATACTGT 966  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 127 GCCATCTGAGGAAACACATTATGGATTCAGTAAGTCACTTCAC 186  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 965 GCCATCTGAGGAAACACATTATGGATTCAGTAAGTCACTTCAC 186  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 187 GCTACTTCAAGAAGTGTACTGTGCTGGAACTCTGTAACCATGCTTCACTTCAC 246  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 905 GCTACTTCAAGAAGTGTACTGTGCTGGAACTCTGTAACCATGCTTCACTTCAC 846  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 247 TGCAATCTGCTGGCTCAAACACGACAGCTGGTGTCAATTGGACAACAGAGTGGAA 306  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 252 TGCAATCTGCTGGCTCAAACACGACAGCTGGTGTCAATTGGACAACAGAGTGGAA 193  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 307 TTCCAAAAGTATGGGCACTAG 327  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 192 TTCCAAAAGTATGGGCACTAG 172  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 307 TTCCAAAAGTATGGGCACTAG 327  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Query 785 TTCCAAAAGTATGGGCACTAG 765  
 CC Best Local Similarity 100.0%; Prod. No. 2.9e-154;  
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ RESULT 11  
 CC ID ACN90161 standard; DNA; 4543 BP.  
 CC AC ACN90161;  
 CC XX

ADQ92179 ID ADQ92179 standard; DNA; 503 BP. XX AC ADQ92179; XX DT 07-OCT-2004 (first entry) XX DE Human autoantigen DNA fragment MPMgp800L05536. XX ds; autoantigen; antibody; hybridoma; biosensor chip; extracorporeal differential diagnosis; autoimmune disease; ribosomal protein; tubulin; dolichyl-diphospho-oligosaccharide-glycosyl transferase; multiple sclerosis; rheumatoid arthritis; epitope mapping; affinity chromatography; electrophoresis; autoantibody apheresis; RNA interference; RNAi. XX OS Homo sapiens. XX PN WO2004058972-A1. XX PD 15-JUL-2004. XX PP 23-DEC-2002; 2002WO-EP014731. XX PR 23-DEC-2002; 2002WO-EP014731. XX PA (THIE) THIESSEN H. PA (LORE) LORENZ P. XX PT Thiesen H., Lorenz P.; DR 2004-543459/52. XX PT New human DNA autoantigens, useful as assay, diagnostic, and prognostic reagents and for treating autoimmune disease, also related expression products and antibodies with similar uses. XX PS Claim 1; SEQ ID NO 160; 110pp; German. XX CC This invention describes novel human DNA autoantigens which are used to CC produce recombinant expression vectors; prokaryotic or eukaryotic cells; CC poly- or mono-clonal antibodies (Ab) specific; hybridomas that express CC monoclonal Ab; biosensor chips having an addressable sequence pattern as CC medical or diagnostic instruments that include the biosensor; for CC extracorporeal differential diagnosis of autoimmune diseases and CC predisposition to them. The autoantigen polynucleotides encode ribosomal CC proteins; tubulins; dolichyl-diphospho-oligosaccharide glycosyl CC transferases and proteins. The antibodies may be labelled conventionally CC with radioisotopes, coloured or fluorescent groups, or a member of the CC biocinavidin pair, or colloidal gold. The autoantigens can be directed CC against mitochondria, liver-kidney microsomes; histidyl-tRNA; nuclear CC membrane; neutrophilic cytoplasm; insect cells; epidermal intracellular CC or basal membrane antigens; Golgi or cell nuclei, or associated with CC multiple sclerosis or rheumatoid arthritis. They are useful for epitope CC mapping; in affinity chromatography or electrophoresis; for diagnosis, CC prognosis, control of treatment or therapeutic diagnosis of autoimmune CC diseases, particularly in vitro differential diagnosis of autoimmune CC diseases; to produce biosensor chips or for autoantibody apheresis. CC Autoantigen DNA can be used for therapeutic RNA interference against CC autoantibodies. Biochips that carry the new materials are useful in CC medical and diagnostic instruments. ADQ92020-ADQ92280 represent human CC autoantigens. XX Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other; SQ Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other; Query Match 97.9%; Score 320; DB 12; Length 503; Best Local Similarity 100.0%; Pred. No. 1e-153; O.; Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 8 CAGCGATGGATGTGGATACCCGAGGCCAACGGCAAGAAGGGCTTG 67 db 1 CAGCGATGGATGTGGATACCCGAGGCCAACGGCAAGAAGGGCTTG 60	QY 68 AAGTAAAAAGTGGAAATCAGTAGCCCTCTGGGCTGGCCCTGGGATATTGTGGTTGATAACTCTG 127 Db 61 AACGTAAAAGTGGAAATCAGTAGGCCCTCTGGGCTGGGATATTGTGGTTGATAACTCTG 120 QY 128 CCATCTGCAGGAACACATTATGGATCTTGCATAGAATGTCAAAGCTAACCGGGTCGG 187 Db 121 CCATCTGCAGGAACACATTATGGATCTTGCATAGAATGTCAAAGCTAACCGGGTCGG 180 QY 188 CTACTTCAGAAGAGGTGACTGTGCTGGGACTGTGTAACCATGCTTTTCACTTCCACT 247 Db 181 CTACTTCAGAAGAGGTGACTGTGCTGGGACTGTGTAACCATGCTTTTCACTTCCACT 240 QY 248 GCATCTCNGCNGCTCAAACAGCACAGGTGTGCTGGACAAAGAGAGGGAT 307 Db 241 GCATCTCNGCNGCTCAAACAGCACAGGTGTGCTGGACAAAGAGAGGGAT 300 QY 308 TCCAAAAGTATGGCCACTAG 327 Db 301 TCCAAAAGTATGGCCACTAG 320	QY RESULT 12 Db ABV25615/C ID ABV25615 standard; cDNA; 4476 bp. XX AC ABV25615; XX DT 16-SEP-2002 (first entry) XX DB Human prostate expression marker cDNA 25606. XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker; KW pharmacogenomic marker; gene; ss. XX OS Homo sapiens. XX PN WO2001608860-A2. XX PD 23-AUG-2001. XX PR 20-FEB-2001; 2001WO-US005171. XX PR 17-FEB-2000; 2000US-0183319P. PR 16-MAR-2000; 2000US-0189862P. PR 25-MAY-2000; 2000US-0207454P. PR 09-JUN-2000; 2000US-0211314P. PR 18-JUL-2000; 2000US-0219007P. PR 13-DEC-2000; 2000US-0255281P.	XX Schlegel R, Endege WO, Monahan JE; XX WPI; 2001-662795/76.	XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer. XX Claim 1; Page 5119-5120; 11750pp; English. XX (MILL-) MILLENIUM PREDICTIVE MEDICINE INC. XX PA The invention relates to an isolated nucleic acid molecule (I) comprising CC a nucleotide sequence given in Tables 1-9 (ABV0001-ABV62213) of the CC specification or its complement. (I) is useful for: (a) assessing whether CC a patient is afflicted with prostate cancer; (b) monitoring the CC progression of prostate cancer in a patient; (c) assessing the efficacy CC of a test compound to inhibit prostate cancer in a patient; (d) assessing CC the efficacy of a therapy for inhibiting prostate cancer in a patient; CC (e) selecting a composition for inhibiting prostate cancer in a patient; CC (f) assessing the prostate cell carcinogenic potential of a compound; (g) CC determining whether prostate cancer has metastasized in a patient; (h) CC assessing the aggressiveness or indolence of prostate cancer in a patient;
---	---	--	--	--

CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX Sequence 4476 BP; 1085 A; 1129 C; 1015 G; 1247 T; 0 U; 0 Other;  
 SQ Query Match 94.2%; Score 308; DB 5; Length 4476;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-147;  
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7 GCAGCGATGGATGTGGATAACCCGAGGGACCAACAGGGCGGCCAAGAACGGCTT 66  
 Db 1014 GCAGCGATGGATGTGGATAACCCGAGGGACCAACAGGGCGGCCAAGAACGGCTT 955  
 Qy 67 GAAGTGA AAAAGTGGAAATGCAAGTAGCCTCTGGGCTGGSATATGTGGTTGATAACTGT 126  
 Db 954 GAAGTGA AAAAGTGGAAATGCAAGTAGCCTCTGGGCTGGSATATGTGGTTGATAACTGT 895  
 Qy 127 GCCATCTGCAGGAACCAATTGGATCTTGATAGAATGCAAGCTAACAGGGTCCC 186  
 Db 894 GCCATCTGCAGGAACCAATTGGATCTTGATAGAATGCAAGCTAACAGGGTCCC 835  
 Qy 187 GCTACTTCAGAAGAGTGTACTGTGGCATGGGAGTCTGTAAACCATGTTTCACTTCAC 246  
 Db 834 GCTACTTCAGAAGAGTGTACTGTGGCATGGGAGTCTGTAAACCATGTTTCACTTCAC 775  
 Qy 247 TGCAATCTCGCTGCTGCTCAAAAACGACAAGCAGGTGGAA 306  
 Db 714 TTCCAAAAA 707  
 Qy 307 TTCCAAAAA 314  
 Db 714 TTCCAAAAA 707

RESULT 13  
 ACL57420 ID ACL57420 standard; cDNA; 311 BP.  
 AC ACL57420;  
 XX DT 24-MAR-2005 (first entry)  
 DE Human colon cancer differentially expressed polynucleotide, SEQ ID:3555.  
 XX KW Differential expression; diagnosis; therapy; drug screening; cancer;  
 neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;  
 SS.  
 XX OS Homo sapiens.  
 PN WO2005000087-A2.  
 XX PD 06-JAN-2005.  
 PF 13-MAY-2004; 2004WO-US015421.  
 XX PR 03-JUN-2003; 2003US-0475872P.  
 XX PA (CHIR ) CHIRON CORP.  
 PT New isolated polynucleotides, which are differentially expressed in colon  
 cancer cell, useful for treating cancer, e.g. colon cancer, breast  
 cancer, or pancreatic cancer.  
 XX PS Claim 1; SEQ ID NO 3555; 97pp; English.

XX by detection of a gene product of the polynucleotides; a method for  
 CC inhibiting a cancerous phenotype of a cell by inhibiting a gene product  
 CC of the polynucleotides; a method of treating an individual with cancer by  
 CC administration of a modulator of a gene product of the polynucleotides;  
 CC and an isolated antibody that specifically binds to a polypeptide encoded  
 CC by one of the 9672 polynucleotides. The polynucleotides, polypeptides,  
 CC antibodies, and methods are useful for the detection of cancerous cells;  
 CC identification of agents that modulate the phenotype of cancerous cells;  
 CC for the identification of therapeutic targets for cancer chemotherapy;  
 CC and for the treatment of cancer, especially colon cancer and metastasized  
 CC colon cancer, but also breast or pancreatic cancer. The polynucleotides  
 CC are also useful as a source of probes or primers for use in diagnostic  
 CC methods. The differentially expressed polynucleotides or their encoded  
 CC proteins can additionally be used as vaccines to modulate primary immune  
 CC responses for the prevention or treatment of cancer. The present sequence  
 CC represents a specifically claimed polynucleotide which is differentially  
 CC expressed in colon cancer. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 311 BP; 77 A; 75 C; 87 G; 72 T; 0 U; 0 Other;  
 Query Match 90.5%; Score 296; DB 14; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 2.e-141;  
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATGGCGAGCGATGGATGTGGATACCCGAGGGCACCACAGGGCGGCCAAGAACGG 60  
 Db 16 ATGGCGAGCGATGGATGTGGATACCCGAGGGCACCACAGGGCGGCCAAGAACGG 75  
 Qy 61 CGCTTGAACTGAAAAAAGTGGAAATGCACTGAGCCCCCTCTGGGATATTGGTTGTAT 120  
 Db 76 CGCTTGAAAGTGAAGAAATGGAAATGCACTGAGCCCCCTCTGGGATATTGGTTGTAT 135  
 Qy 121 AACGTGCGCATCTCGAGAACCATATTGGATCTGGATAGAATGTCAGCTAACCG 180  
 Db 136 AACGTGCGCATCTCGAGAACCATATTGGATCTGGATAGAATGTCAGCTAACCG 195  
 Qy 181 GCGTCCGCTACTTCAAGAGTGTACTGTGGCATGGGAGTCTGTAAACATGCTTCAC 240  
 Db 196 GCGTCCGCTACTTCAAGAGTGTACTGTGGCATGGGAGTCTGTAAACATGCTTCAC 255  
 Qy 241 TTCCACTGCACTCTCGCTGGCTCAAAACGACAGGTGTCTGGACAAACAG 296  
 Db 256 TTCCACTGCACTCTCGCTGGCTCAAAACGACAGGTGTCTGGACAAACAG 311

RESULT 14  
 ADF42703\_c ID ADF42703 standard; cDNA; 3484 BP.  
 AC ADF42703;  
 XX DT 26-FEB-2004 (first entry)  
 XX DE Human Testicon-1 nucleotide sequence SEQ ID NO:9.  
 KW KW diabetic; pre-diabetic; Type 2 diabetes; antidiabetic; gene therapy;  
 diabetes; insulin resistance; metabolic disease; human; gene; ss.  
 XX OS Homo sapiens.  
 XX PN WO2003102163-A2.  
 XX PD 11-DEC-2003.  
 PF 04-JUN-2003; 2003WO-US017825.  
 XX PN WO2003102163-A2.  
 PF 04-JUN-2002; 2002US-0385857P.  
 PR 04-JUN-2002; 2002US-0386013P.  
 PR 04-JUN-2002; 2002US-0386074P.

CC The invention relates to 9672 polynucleotides (ACL53866 - ACL63337) which  
 CC are differentially expressed in colon cancer cells. The invention also  
 CC relates to vectors and host cells comprising a differentially expressed  
 CC polynucleotide of the invention; a method for detecting a cancerous cell

PR	04-JUN-2002; 2002US-0386107P.	Db	236 GAA GTG AAA AGT GGA AT GCA GT AG TGG CCG TGG GAT AT TGT GGT GAT AACT GT 177
PR	05-JUN-2002; 2002US-0386314P.	Qy	127 GCC AT CTG CAG GAC CAAT TAT GAT CTT TGC AT TGC TAAG TCA AG TCA ACC CGC GTC CC 186
PR	05-JUN-2002; 2002US-0386326P.	Db	176 GCC AT CTG CAG GAC CAAT TAT GAT CTT TGC AT TGC TAAG TCA AG TCA ACC CGC GTC CC 117
PR	05-JUN-2002; 2002US-0386332P.	Qy	187 GCT ACT TCA GAA AGT GTG TACT GTG CAT GTG GGA GTG CTG TAAC AT GCT TT CAC TT CAC 246
PR	05-JUN-2002; 2002US-0386481P.	Db	116 GCT ACT TCA GAA AGT GTG TACT GTG CAT GTG GGA GTG CTG TAAC AT GCT TT CAC TT CAC 57
PR	05-JUN-2002; 2002US-0386512P.	Qy	247 TGC ACT CTG CTC GCT GGT GCT CATT GG CAAC AGA GAG GTG 302
PR	05-JUN-2002; 2002US-0386558P.	Db	56 TGC ACT CTG CTC GCT GGT GCT CATT GG CAAC AGA GAG GTG 1
PR	05-JUN-2002; 2002US-0386600P.		
PR	05-JUN-2002; 2002US-0386615P.		
PR	05-JUN-2002; 2002US-0386654P.		
PR	06-JUN-2002; 2002US-0386838P.		
PR	06-JUN-2002; 2002US-0386867P.		
PR	06-JUN-2002; 2002US-0386944P.		
PR	06-JUN-2002; 2002US-0386955P.		
PR	06-JUN-2002; 2002US-0387017P.		
PR	06-JUN-2002; 2002US-0387026P.		
PR	20-JUN-2002; 2002US-0387039P.		
XX			
PA-)	METABOLEX INC.	RESULT 15	
PA	Allan B, Gregoire F, Lavan B, Moodie S, Waters S, Wong C;	ADQ18564/c	
PT		ID ADQ18564 standard; DMR; 3484 BP.	
XX		XX	
DR		XX	Human soft tissue sarcoma-upregulated DNA - SEQ ID 1383.
XX		XX	
PR	Identifying an agent for treating diabetic or pre-diabetic individuals	KW	soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
PR	comprises contacting an agent with a polypeptide, e.g., human ceramidase,	OS	
PR	and selecting an agent that modulates the expression or activity of the	XX	
PR	polypeptide.	PN	W02004048938-A2.
XX		XX	
PS	Disclosure; SEQ ID NO 9; 209pp; English.	PD	10-JUN-2004.
XX		XX	
CC	The present invention describes a method for identifying an agent for	XX	26-AUG-2004 (First entry)
CC	treating a diabetic or pre-diabetic individual. The method comprises	DT	
CC	contacting an agent to a mixture comprising a polypeptide encoded by a	XX	
CC	nucleic acid that hybridises under stringent conditions to a nucleic acid	DE	
CC	encoding any of the 23 fully defined amino acid sequences given in the	XX	
CC	specification, and selecting an agent that modulates the expression or	XX	
CC	activity of the polypeptide. Also described: (1) a method of treating a	XX	
CC	diabetic or pre-diabetic animal, comprising administering to the animal a	XX	
CC	therapeutic amount of an agent identified by the method described above;	XX	
CC	(2) a method of introducing an expression cassette into a cell,	XX	
CC	comprising introducing into the cell a polynucleotide encoding a polypeptide,	XX	
CC	promoter operably linked to a polynucleotide encoding a polypeptide,	XX	
CC	where the polynucleotide hybridises under stringent conditions to a	XX	
CC	nucleic acid encoding the above amino acid sequences; and (3) a method of	XX	
CC	diagnosing an individual who has Type 2 diabetes or is pre-diabetic,	XX	
CC	comprising detecting in a sample from the individual the level of a	XX	
CC	polypeptide or the level of the above-mentioned polynucleotide encoding	XX	
CC	the polypeptide, where a modulated level of the polypeptide or	XX	
CC	polynucleotide in the sample compared to a level of the polypeptide or	XX	
CC	polynucleotide in either a lean individual or a previous sample from the	XX	
CC	individual indicates that the individual is diabetic or pre-diabetic. The	XX	
CC	method is useful in diagnosing and treating diabetes, insulin resistance	XX	
CC	or related metabolic diseases in human subjects. The method may also be	XX	
CC	used in identifying agents for treating diabetic or pre-diabetic	XX	
CC	individuals. The present sequence is used in the exemplification of the	XX	
CC	present invention.	XX	
SQ	Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;	PS	Example 2; SEQ ID NO 1383; 210pp; English.
Query Match	90.5%; Score 296; DB 12; Length 3484;	XX	XX
Best Local Similarity	100.0%; Pred. No. 2e-141;	CC	The invention relates to a novel method for detecting soft tissue sarcoma
Matches	0; Mismatches 0;	CC	which comprises obtaining a first soft tissue sample from an individual
2396;	Conservative	CC	and normal soft tissue sample from the same or different individual,
Db	7 GCAGCGATGCGATGTCGATACCCGAGCCACACGCCGGAGAGGGCTT 66	CC	determining the expression of a gene in both samples and comparing the
Qy	67 GAAGTGAAGAAAAGTGGAAATGCACTGGCCCTCTGGGCCTGGATATTGGCTTGATAACTGT 126	CC	expression of the gene in both soft tissue samples, where a higher level
Qy	296 GCACCGATGCGATGTCGATACCCGAGCCACACGCCGGAGAGGGCTT 237	CC	of protein expression in the first soft tissue sample indicates the
Qy	7 GCACCGATGCGATGTCGATACCCGAGCCACACGCCGGAGAGGGCTT 66	CC	presence of soft tissue sarcoma. The method of the invention has
Qy	90.5%; Score 296; DB 12; Length 3484;	CC	cystostatic applications and may be useful for detecting soft tissue
Best Local Similarity	100.0%; Pred. No. 2e-141;	CC	sarcoma, possibly via gene therapy or vaccine production. The nucleic
Matches	0; Mismatches 0;	CC	acid sequences may be useful in diagnostic and screening applications.
SQ	Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;	CC	The current sequence is that of a human soft tissue sarcoma-upregulated
Query Match	90.5%; Score 296; DB 12; Length 3484;	CC	CC DNA of the invention. The current sequence is not shown within the
Best Local Similarity	100.0%; Pred. No. 2e-141;	CC	CC specification per se but was submitted in CD format by the inventor.
Matches	0; Mismatches 0;	CC	XX
SQ	Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;	CC	Query Match 90.5%; Score 296; DB 12; Length 3484;
Qy	7 GCAGCGATGCGATGTCGATACCCGAGCCACACGCCGGAGAGGGCTT 66	CC	Best Local Similarity 100.0%; Pred. No. 2e-141;
Db	296 GCACCGATGCGATGTCGATACCCGAGCCACACGCCGGAGAGGGCTT 237	CC	Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	7 GCACCGATGCGATGTCGATACCCGAGCCACACGCCGGAGAGGGCTT 66	CC	XX

Db	296	GCAGGGATGGATGTGGATAACCCGAGGGACCAAACAGCGGGCGGGCAAGAACGGCTT	237
QY	67	GAAGTGA AAAAAGTGGAAATGCA GTAGCTAGCCCTCTGGGCTGGATAATTGGGTTGATAACTGT	126
Db	236	GAAGTGA AAAAAGTGGAAATGCA GTAGCTAGCCCTCTGGGCTGGATAATTGGGTTGATAACTGT	177
QY	127	GCCATCTGCA GGAACCA CATTATGGATCTTGCA TAGAAGTCAGCTAACAGCGGTCC	186
Db	176	GCCATCTGCA GGAACCA CATTATGGATCTTGCA TAGAATGTCAGCTAACAGCGGTCC	117
QY	187	GCTACTTCA GAGA GAGTGTACTGTGCA TGGGAGCTGTACCATGCTTTCACTTCAC	246
Db	116	GCTACTTCA GAGA GAGTGTACTGTGCA TGGGAGCTGTACCATGCTTTCACTTCAC	57
QY	247	TGCATCTCTCCTGGCTAA AACACCA CAGTGTCACATGGACAACAGAGATG	302
Db	56	TGCATCTCTGCTGGCTAA AACACCA CAGTGTCACATGGACAACAGAGATG	1

Search completed: March 8, 2006, 16:12:25  
Job time : 372.547 secs

1885 Page Blank (uspi)



ORIGIN	FORKYGH"							
Query Match	100.0% ; Score 327; DB 8; Length 327;							
Best Local Similarity	100.0% ; Pred. No. 3.5e-184;							
Matches 327; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;							
Qy	1 ATGGCGGCAAGCGATGGATGTGGATAACCCCGAGGGCACCAACAGGGGGCAAGAG 60							
Db	1 ATGGCGGCAAGCGATGGATGTGGATAACCCGGAGGGCACCAACAGGGGGCAAGAG 60							
Qy	61 CGCTTTGAGTGAAAGGTGGAATGGTGAAGTCAGTAGCCCTGGGATATTGGTTGAT 120							
Db	61 CGCTTTGAGTGAAAGGTGGAATGGTGAAGTCAGTAGCCCTGGGATATTGGTTGAT 120							
Qy	121 AACCTGTGCCATTCTCGAGAACCATTTGATCTTGGATAGAATGTAAGCTAACAG 180							
Db	121 AACCTGTGCCATTCTCGAGAACCATTTGATCTTGGATAGAATGTAAGCTAACAG 180							
Qy	181 GCGTCCGCCATCTACTTCAAGAGTGTACTTCAAGTGTGATGGATCTTGTAC 240							
Db	181 GCGTCCGCCATCTACTTCAAGAGTGTACTTCAAGTGTGATGGATCTTGTAC 240							
Qy	241 TTCACTGTGATCTCTCGTGGCTAAACAGACAGGTGTCCATTGGCAACAGAG 300							
Db	241 TTCACTGTGATCTCTCGTGGCTAAACAGACAGGTGTCCATTGGCAACAGAG 300							
Qy	301 TGGGAATTCCAAAAGTATGGCACTAG 327							
Db	301 TGGGAATTCCAAAAGTATGGCACTAG 327							
RESULT 2								
LOCUS	CQ698451	433 bp	DNA					
DEFINITION	Sequence 43377 from Patent WO02070737.							
VERSION	CQ698451							
KEYWORDS	CQ698451.1 GI:42252856							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE	1 Liew, C.C., Marshall, W.E. and Zhang, H. Compositions and methods relating to osteoarthritis Patent: WO 02070737-A 3505 12-SEP-2002;							
AUTHORS	Liew, C.C., Marshall, W.E. and Zhang, H.							
TITLE	Compositions and methods relating to osteoarthritis							
JOURNAL	Patent: WO 02070737-A 43377 12-SEP-2002;							
FEATURES	Location/Qualifiers							
source	1. .433 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"							
ORIGIN								
Query Match	100.0% ; Score 327; DB 6; Length 453;							
Best Local Similarity	100.0% ; Pred. No. 3.5e-184;							
Matches 327; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;							
Qy	1 ATGGCGGCAAGCGATGGATGTGGATAACCCCGAGGGCACCAACAGGGGGCAAGAG 60							
Db	1 ATGGCGGCAAGCGATGGATGTGGATAACCCCGAGGGCACCAACAGGGGGCAAGAG 60							
Qy	61 CGCTTGAGTGAAAGGTGGAATGGTGAAGTCAGTAGCCCTGGGATATTGGTTGAT 120							
Db	61 CGCTTGAGTGAAAGGTGGAATGGTGAAGTCAGTAGCCCTGGGATATTGGTTGAT 120							
Qy	80 CGCTTGAGTGAAAGGTGGAATGGTGAAGTCAGTAGCCCTGGGATATTGGTTGAT 139							
Db	80 CGCTTGAGTGAAAGGTGGAATGGTGAAGTCAGTAGCCCTGGGATATTGGTTGAT 139							
Qy	121 AACCTGTGCCATTCTCGAGAACCATTTGATCTTGGATAGAATGTAAGCTAACAG 180							
Db	121 AACCTGTGCCATTCTCGAGAACCATTTGATCTTGGATAGAATGTAAGCTAACAG 180							
Qy	140 AACCTGTGCCATTCTCGAGAACCATTTGATCTTGGATAGAATGTAAGCTAACAG 199							
Db	140 AACCTGTGCCATTCTCGAGAACCATTTGATCTTGGATAGAATGTAAGCTAACAG 199							
RESULT 4								
LOCUS	CQ695007	467 bp	DNA					
DEFINITION	Sequence 39933 from Patent WO02070737.							
VERSION	CQ695007							
KEYWORDS	CQ695007.1 GI:42240530							
SOURCE	Homo sapiens (human)							

ORGANISM	Homo sapiens	Qy	1 ATGGGGCAGGATGGATGGTACCCGGACCAACGGGGGGAAAGAG
	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE			
AUTHORS	Liew, C.C., Marshall, W.E. and Zhang, H.		
TITLE	Compositions and methods relating to osteoarthritis		
JOURNAL	Patent: WO 0207037-A 39933 12-SEP-2002;		
	Chondrogen Inc. (CA)		
FEATURES	Location/Qualifiers		
source	1. .467 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:5606"		
ORIGIN			
Query Match	Score 327; DB 6; Length 467;	Qy	241 TTCACTGATCTCGTGGCTAACAGGAGGTGTCAATTGGACAAAGAG 300
Best Local Similarity	100.0%; Pred. No. 3.6e-184;		
Matches	327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	257 TTCACTGATCTCGTGGCTAACAGGAGGTGTCAATTGGACAAAGAG 316
Qy	1 ATGGGGCAGGATGGATGGTACCCGGAGCACCACAGGGCGGGAAAGAG 60	Qy	301 TGGGAATCCAAAGTATGGCACTAG 327
Db	20 ATGGGGCAGGATGGATGGTACCCGGAGCACCACAGGGCGGGAAAGAG 79	Db	317 TGGGAATCCAAAGTATGGCACTAG 343
Qy	61 CGRTTGAACTGAAAGTGAATGAACTGAACTGAACTGAAATGGTTGAT 120		
Db	80 CGRTTGAACTGAAAGTGAATGAACTGAACTGAACTGAAATGGTTGAT 139		
Qy	121 AACGTGCCATCTGGAGAACCATTAATGGATCTTGGATAAGGTAACAG 180		
Db	140 AACGTGCCATCTGGAGAACCATTAATGGATCTTGGATAAGGTAACAG 199		
Qy	181 GGTCGGTACTCTGGAGAAGTGTACTGGCATGGGGGTCTGTAACCATGCTTAC 240		
Db	200 GGTCGGTACTCTGGAGAAGTGTACTGGCATGGGGGTCTGTAACCATGCTTAC 259		
Qy	241 TTCACTGATCTCGTGGCTAACAGGAGGTGTCAATTGGACAAAGAG 300		
Db	260 TTCACTGATCTCGTGGCTAACAGGAGGTGTCAATTGGACAAAGAG 319		
Qy	301 TGGGAATCCAAAGTATGGCACTAG 327		
Db	320 TGGGAATCCAAAGTATGGCACTAG 346		
RESULT	6		
LOCUS	CQ711142	LOCUS	CQ711142
DEFINITION	Sequence 56068 from Patent WO0207037.	DEFINITION	Sequence 56068 from Patent WO0207037.
ACCESSION	CQ711142	ACCESSION	CQ711142
VERSION	CQ711142.1	VERSION	CQ711142.1
KEYWORDS		KEYWORDS	GI:42271999
SOURCE		SOURCE	
ORGANISM	Homo sapiens (human)	ORGANISM	Homo sapiens
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE		REFERENCE	
AUTHORS	Liew, C.C., Marshall, W.E. and Zhang, H.	AUTHORS	Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE	Compositions and methods relating to osteoarthritis	TITLE	Compositions and methods relating to osteoarthritis
JOURNAL	Patent: WO 0207037-A 56068 12-SEP-2002;	JOURNAL	Patent: WO 0207037-A 56068 12-SEP-2002;
	Chondrogen Inc. (CA)		
FEATURES	Location/Qualifiers	FEATURES	Location/Qualifiers
source	1. .472 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	source	1. .472 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
ORIGIN		ORIGIN	
Query	Match 100.0%; Score 327; DB 6; Length 472;	Query	Match 100.0%; Score 327; DB 6; Length 472;
	Best Local Similarity 100.0%; Pred. No. 3.6e-184;		Best Local Similarity 100.0%; Pred. No. 3.6e-184;
	Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATGGGGCAGGATGGATGGTACCCGGAGCACCACAGGGCGGGAAAGAG 60	Qy	1 ATGGGGCAGGATGGATGGTACCCGGAGCACCACAGGGCGGGAAAGAG 60
Db	20 ATGGGGCAGGATGGATGGTACCCGGAGCACCACAGGGCGGGAAAGAG 79	Db	20 ATGGGGCAGGATGGATGGTACCCGGAGCACCACAGGGCGGGAAAGAG 79
Qy	61 CGRTTGAACTGAAAGTGAATGAACTGAACTGAACTGAAATGGTTGAT 120	Qy	61 CGRTTGAACTGAAAGTGAATGAACTGAACTGAACTGAAATGGTTGAT 120
Db	80 CGRTTGAACTGAAAGTGAATGAACTGAACTGAACTGAAATGGTTGAT 139	Db	80 CGRTTGAACTGAAAGTGAATGAACTGAACTGAACTGAAATGGTTGAT 139
Qy	121 AACGTGCCATCTGGAGAACCATTAATGGATCTTGGATAAGGTAACAG 180	Qy	121 AACGTGCCATCTGGAGAACCATTAATGGATCTTGGATAAGGTAACAG 180
Db	140 AACGTGCCATCTGGAGAACCATTAATGGATCTTGGATAAGGTAACAG 199	Db	140 AACGTGCCATCTGGAGAACCATTAATGGATCTTGGATAAGGTAACAG 199
Qy	181 GGTCGGTACTCTGGAGAAGTGTACTGGCATGGGGGTCTGTAACCATGCTTAC 240	Qy	181 GGTCGGTACTCTGGAGAAGTGTACTGGCATGGGGGTCTGTAACCATGCTTAC 240
Db	200 GGTCGGTACTCTGGAGAAGTGTACTGGCATGGGGGTCTGTAACCATGCTTAC 259	Db	200 GGTCGGTACTCTGGAGAAGTGTACTGGCATGGGGGTCTGTAACCATGCTTAC 259
Qy	241 TTCACTGATCTCGTGGCTAACAGGAGGTGTCAATTGGACAAAGAG 300	Qy	241 TTCACTGATCTCGTGGCTAACAGGAGGTGTCAATTGGACAAAGAG 300
Db	260 TTCACTGATCTCGTGGCTAACAGGAGGTGTCAATTGGACAAAGAG 319	Db	260 TTCACTGATCTCGTGGCTAACAGGAGGTGTCAATTGGACAAAGAG 319
Qy	301 TGGGAATCCAAAGTATGGCACTAG 327	Qy	301 TGGGAATCCAAAGTATGGCACTAG 327
Db	320 TGGGAATCCAAAGTATGGCACTAG 346	Db	320 TGGGAATCCAAAGTATGGCACTAG 346
RESULT	5		
LOCUS	CQ712328	LOCUS	CQ712328
DEFINITION	Sequence 57254 from Patent WO0207037.	DEFINITION	Sequence 57254 from Patent WO0207037.
ACCESSION	CQ712328	ACCESSION	CQ712328
VERSION	CQ712328.1	VERSION	CQ712328.1
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM	Homo sapiens (human)	ORGANISM	Homo sapiens
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE		REFERENCE	
AUTHORS	Liew, C.C., Marshall, W.E. and Zhang, H.	AUTHORS	Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE	Compositions and methods relating to osteoarthritis	TITLE	Compositions and methods relating to osteoarthritis
JOURNAL	Patent: WO 0207037-A 57254 12-SEP-2002;	JOURNAL	Patent: WO 0207037-A 57254 12-SEP-2002;
	Chondrogen Inc. (CA)		
FEATURES	Location/Qualifiers	FEATURES	Location/Qualifiers
source	1. .471 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:5606"	source	1. .471 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:5606"
ORIGIN		ORIGIN	
Query	Match 100.0%; Score 327; DB 6; Length 471;	Query	Match 100.0%; Score 327; DB 6; Length 471;
	Best Local Similarity 100.0%; Pred. No. 3.6e-184;		Best Local Similarity 100.0%; Pred. No. 3.6e-184;
	Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
 TITLE *peptides, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof*  
 Patent: WO 02068579-A 15833 06-SEP-2002;  
 PE Corporation (NY) (US)

FEATURES Location/Qualifiers  
 source 1. 507  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query	Match	Score	DB	Length
QY	ATGGCGCAGGGATGTGATAACCGGGACCAACAGCGGGCGGGAAAGAAG	327	6	507;
Db	ATGGCGCAGGGATGTGATAACCGGGACCAACAGCGGGCGGGAAAGAAG	327	0	0;
QY	CGCTTGAAGTGAAGAAGGTGAAATGCAATGCCGAGCTGGATTCAGCTGG	120	0	0;
Db	CGCTTGAAGTGAAGAAGGTGAAATGCAATGCCGAGCTGGATTCAGCTGG	126	0	0;
QY	ACTGTCGCCATTGCGAGAACCATATTGATCTTGATAGATGTAACAG	180	0	0;
Db	ACTGTCGCCATTGCGAGAACCATATTGATCTTGATAGATGTAACAG	186	0	0;
QY	GCGTCCGCTACTTCAGAAGACTGTACTGTCCATGGAGCTGTAAACC	240	0	0;
Db	GCGTCCGCTACTTCAGAAGACTGTACTGTCCATGGAGCTGTAAACC	246	0	0;
QY	TTCGACTGCATCTCGCTGCTCAAACAGCACGGTGCTCATTGGACA	300	0	0;
Db	TTCGACTGCATCTCGCTGCTCAAACAGCACGGTGCTCATTGGACA	306	0	0;
QY	TGGGAATTCCAAGTAGTGGCACTAG	327		
Db	TGGGAATTCCAAGTAGTGGCACTAG	333		

RESULT 10  
 BD271520 LOCUS BD271520 508 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Von Hippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase.  
 ACCESSION BD271520  
 VERSION BD271520.1 GI:33081288  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Hominidae; Homo; Eutheria; Euarchontoglires; Primates; Catarhini;  
 Conaway,J.W.; Conaway,R.C. and Kamura,T.

REFERENCE JOURNAL  
 AUTHORS OKLAHOMA MEDICAL RESEARCH FOUNDATION  
 TITLE Von Hippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase  
 Patent: JP 200254175-A 1 10-DEC-2002;  
 COMMENT OS Homo sapiens (human)  
 PN JP 200254175-A/1  
 PD 10-DEC-2002  
 PF 25-FEB-2000 JP 2000601023  
 PR 26-FEB-1999 US 60121787  
 PI JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA, PC  
 C12N15/09, A61K38/00, A61K38/53, A61K45/00, A61P35/00, C07K14/47, PC  
 C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12P21/02, G01N33/15, G01N33/ PC  
 50, G01N33/68

AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
 TITLE *Von Hippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase*  
 Patent: WO 02068579-A 15833 06-SEP-2002;  
 PE Corporation (NY) (US)

FEATURES Location/Qualifiers  
 source 1. 508  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query	Match	Score	DB	Length
QY	ATGGCGCAGGGATGTGATAACCGGGACCAACAGCGGGCGGGAAAGAAG	327	6	508;
Db	ATGGCGCAGGGATGTGATAACCGGGACCAACAGCGGGCGGGAAAGAAG	327	0	0;
QY	CGCTTGAAGTGAAGAAGGTGAAATGCAATGCCGAGCTGGATTCAGCTGG	120	0	0;
Db	CGCTTGAAGTGAAGAAGGTGAAATGCAATGCCGAGCTGGATTCAGCTGG	126	0	0;
QY	ACTGTCGCCATTGCGAGAACCATATTGATCTTGATAGATGTAACAG	180	0	0;
Db	ACTGTCGCCATTGCGAGAACCATATTGATCTTGATAGATGTAACAG	186	0	0;
QY	GCGTCCGCTACTTCAGAAGACTGTACTGTCCATGGAGCTGTAAACC	240	0	0;
Db	GCGTCCGCTACTTCAGAAGACTGTACTGTCCATGGAGCTGTAAACC	246	0	0;
QY	TTCGACTGCATCTCGCTGCTCAAACAGCACGGTGCTCATTGGACA	300	0	0;
Db	TTCGACTGCATCTCGCTGCTCAAACAGCACGGTGCTCATTGGACA	306	0	0;
QY	TGGGAATTCCAAGTAGTGGCACTAG	327		
Db	TGGGAATTCCAAGTAGTGGCACTAG	333		

RESULT 11  
 AR640603 LOCUS AR640603 508 bp DNA linear PAT 20-APR-2005  
 DEFINITION Sequence 3 from patent US 6858709. Component of von Hippel-Lindau tumor suppressor complex and SCF ubiquitin ligase.  
 ACCESSION AR640603  
 VERSION AR640603.1 GI:62775412  
 KEYWORDS Unknown  
 SOURCE Unknown  
 ORGANISM Unclassified  
 REFERENCE Conaway,J.W.; Conaway,R.C. and Kamura,T.  
 AUTHORS Component of von Hippel-Lindau tumor suppressor complex and SCF ubiquitin ligase.  
 TITLE Patent: US 6858709-A 3 22-FEB-2005;  
 JOURNAL Oklahoma Medical Research Foundation; Oklahoma City, OK  
 FEATURES Location/Qualifiers  
 source 1. 508  
 /organism="unknown"  
 /mol\_type="genomic DNA"  
 ORIGIN

Query	Match	Score	DB	Length
QY	ATGGCGCAGGGATGTGATAACCGGGACCAACAGCGGGCGGGAAAGAAG	327	6	508;
Db	ATGGCGCAGGGATGTGATAACCGGGACCAACAGCGGGCGGGAAAGAAG	327	0	0;
QY	CGCTTGAAGTGAAGAAGGTGAAATGCAATGCCGAGCTGGATTCAGCTGG	120	0	0;
Db	CGCTTGAAGTGAAGAAGGTGAAATGCAATGCCGAGCTGGATTCAGCTGG	126	0	0;
QY	ACTGTCGCCATTGCGAGAACCATATTGATCTTGATAGATGTAACAG	180	0	0;
Db	ACTGTCGCCATTGCGAGAACCATATTGATCTTGATAGATGTAACAG	186	0	0;
QY	GCGTCCGCTACTTCAGAAGACTGTACTGTCCATGGAGCTGTAAACC	240	0	0;
Db	GCGTCCGCTACTTCAGAAGACTGTACTGTCCATGGAGCTGTAAACC	246	0	0;
QY	TTCGACTGCATCTCGCTGCTCAAACAGCACGGTGCTCATTGGACA	300	0	0;
Db	TTCGACTGCATCTCGCTGCTCAAACAGCACGGTGCTCATTGGACA	306	0	0;
QY	TGGGAATTCCAAGTAGTGGCACTAG	327		
Db	TGGGAATTCCAAGTAGTGGCACTAG	333		

Db	67	CGCTTGTGAACTGGAAATGGAAAAAGTGCAATTGCACTTGTGCTGCCTGGATATTGTGTTGAT	Qy	61 CGCTTGTGAACTGGAAATGGAAATGGCAATTGCACTTGTGCTGCCTGGATATTGTGTTGAT 120
Db	121	AACCTGTGCCATTCTCGAGAACCCATTATGATCATTGATGTAAGTCAAGTAACCG	Qy	67 CGCTTGTGAACTGGAAATGGAAATGGCAATTGCACTTGTGCTGCCTGGATATTGTGTTGAT 126
Db	127	AACCTGTGCCATTCTCGAGAACCCATTATGATCATTGATGTAAGTCAAGTAACCG	Qy	121 AACCTGTGCCATTCTCGAGAACCCATTATGATCATTGATGTAAGTCAAGTAACCG 180
Db	181	GCGTCGCTACTTCGAAGAGTGTACTGTGCACTGGGACTCTGTAAACCATGGTTTAC	Qy	127 AACCTGTGCCATTCTCGAGAACCCATTATGATCATTGATGTAAGTCAAGTAACCG 186
Db	187	GCGTCGCTACTTCGAAGAGTGTACTGTGCACTGGGACTCTGTAAACCATGGTTTAC	Qy	181 GCGTCGCTACTTCGAAGAGTGTACTGTGCACTGGGACTCTGTAAACCATGGTTTAC 240
Db	241	TTCACACTGTACTTCGCTGGCTCAAACCGAACAGGTGTCCATTGGACACAAGAG	Qy	187 GCGTCGCTACTTCGAAGAGTGTACTGTGCACTGGGACTCTGTAAACCATGGTTTAC 246
Db	247	TTCACACTGTACTTCGCTGGCTCAAACCGAACAGGTGTCCATTGGACACAAGAG	Qy	241 TTCCACTGCACTCTCGCTGGCTCAAACCGAACAGGTGTCCATTGGACACAAGAG 300
Db	301	TGGGAATTCCAAAAGTAGTGGCACTAG 327	Qy	247 TTCCACTGCACTCTCGCTGGCTCAAACCGAACAGGTGTCCATTGGACACAAGAG 306
Db	307	TGGGAATTCCAAAAGTAGTGGCACTAG 333	Qy	301 TGGGAATTCCAAAAGTAGTGGCACTAG 327
Db	307	TGGGAATTCCAAAAGTAGTGGCACTAG 333	Db	307 TGGGAATTCCAAAAGTAGTGGCACTAG 333
 <b>RESULT 12</b>				
LOCUS	AF140598	AF140598	508 bp	tRNA linear PRI 11-MAY-1999
DEFINITION	Homo sapiens ring-box protein 1 (RBX1) tRNA, complete cds.			
ACCESSION	AF140598	AF140598		
VERSION	1	GI:4769003		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Kamura,T., Koepf,D.M., Conrad,M.N., Skowron,D., Moreland,R.J., Ilionopoulos,C., Lane,W.S., Kaelin,W.G., Jr., Ellidge,S.J., Conaway,R.C., Harper,J.W. and Conaway,J.W.			
AUTHORS	1 (bases 1 to 508)			
TITLE	Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase			
JOURNAL	Science 284 (5414), 657-661 (1999)			
PUBLMED	10213631			
FEATURES	2 (bases 1 to 508)			
AUTHORS	Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.			
TITLE	Direct Submission			
JOURNAL	Submitted (05-APR-1999) Prog. Molec. Cell. Biol., HMMI, Oklahoma Med. Res. Found., 825 NE 13th St., Oklahoma City, OK 73104, USA			
FEATURES	Location/Qualifiers			
REFERENCE	1..508			
gene	/organism="Homo sapiens"			
CDS	/mol type="tRNA"			
	/db_xref="taxon:9606"			
	1..508			
	/gene=RBX1"			
	7..333			
	/gene=RBX1"			
	/note="ring finger-like protein; component of VHL tumor suppressor complex and SCF ubiquitin ligase"			
	/codon_start=1			
	/product="ring-box protein 1"			
	/protein_id="P4AD29715_1"			
	/db_xref="GI:4769004"			
	/translation="MAAADMDDPSGINSAGAKKRFEVKRNNAVALWADIVDNCAICRHIMDLCIECCQANOASATSECTVAVGVCFNRAFHFCISRMILKTRQVCPLLNREWE FQKYGH"			
 <b>ORIGIN</b>				
Query Match	100.0%	Score 327;	DB 8;	Length 508;
Best Local Similarity	100.0%;	Pred. No. 3..6e-184;	Indels 0;	Gaps 0;
Matches 322;	Conservative 0;	Mismatches 0;		
Qy	1 ATGGGGCACCGATGGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Qy	Qy	Qy
Db	7 ATGGGGCACCGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Db	Db	Db
 <b>RESULT 13</b>				
LOCUS	CQ701366	CQ701366	523 bp	DNA
DEFINITION	Sequence 46222 from Patent WO20070737.			
ACCESSION	Q701366			
VERSION	CQ701366.1	GI:42262133		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Liew,C.C., Marshall,W.E. and Zhang,H.			
AUTHORS	Compositions and methods relating to osteoarthritis			
TITLE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
JOURNAL	Patent : WO 03070737-A 46292 12-SEP-2002; Chondrogen Inc. (CA)			
FEATURES	Location/Qualifiers			
source	1..523			
	/mol type="unassigned DNA"			
	/db_xref="taxon:9606"			
 <b>ORIGIN</b>				
Query Match	100.0%;	Score 327;	DB 6;	Length 523;
Best Local Similarity	100.0%;	Pred. No. 3..6e-184;	Indels 0;	Gaps 0;
Matches 327;	Conservative 0;	Mismatches 0;		
Qy	1 ATGGGGCACCGATGGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Qy	Qy	Qy
Db	19 ATGGGGCACCGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Db	Db	Db
 <b>RESULT 14</b>				
LOCUS	CQ701367	CQ701367	523 bp	DNA
DEFINITION	Sequence 46223 from Patent WO20070737.			
ACCESSION	Q701367	GI:42262134		
VERSION	CQ701367.1	GI:42262134		
KEYWORDS				
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Liew,C.C., Marshall,W.E. and Zhang,H.			
AUTHORS	Compositions and methods relating to osteoarthritis			
TITLE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
JOURNAL	Patent : WO 03070737-A 46292 12-SEP-2002; Chondrogen Inc. (CA)			
FEATURES	Location/Qualifiers			
source	1..523			
	/mol type="unassigned DNA"			
	/db_xref="taxon:9606"			
 <b>ORIGIN</b>				
Query Match	100.0%;	Score 327;	DB 6;	Length 523;
Best Local Similarity	100.0%;	Pred. No. 3..6e-184;	Indels 0;	Gaps 0;
Matches 327;	Conservative 0;	Mismatches 0;		
Qy	1 ATGGGGCACCGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Qy	Qy	Qy
Db	19 ATGGGGCACCGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Db	Db	Db
 <b>RESULT 15</b>				
LOCUS	CQ701368	CQ701368	523 bp	DNA
DEFINITION	Sequence 46224 from Patent WO20070737.			
ACCESSION	Q701368	GI:42262135		
VERSION	CQ701368.1	GI:42262135		
KEYWORDS				
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Liew,C.C., Marshall,W.E. and Zhang,H.			
AUTHORS	Compositions and methods relating to osteoarthritis			
TITLE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
JOURNAL	Patent : WO 03070737-A 46292 12-SEP-2002; Chondrogen Inc. (CA)			
FEATURES	Location/Qualifiers			
source	1..523			
	/mol type="unassigned DNA"			
	/db_xref="taxon:9606"			
 <b>ORIGIN</b>				
Query Match	100.0%;	Score 327;	DB 6;	Length 523;
Best Local Similarity	100.0%;	Pred. No. 3..6e-184;	Indels 0;	Gaps 0;
Matches 327;	Conservative 0;	Mismatches 0;		
Qy	1 ATGGGGCACCGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Qy	Qy	Qy
Db	19 ATGGGGCACCGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Db	Db	Db
 <b>RESULT 16</b>				
LOCUS	CQ701369	CQ701369	523 bp	DNA
DEFINITION	Sequence 46225 from Patent WO20070737.			
ACCESSION	Q701369	GI:42262136		
VERSION	CQ701369.1	GI:42262136		
KEYWORDS				
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Liew,C.C., Marshall,W.E. and Zhang,H.			
AUTHORS	Compositions and methods relating to osteoarthritis			
TITLE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
JOURNAL	Patent : WO 03070737-A 46292 12-SEP-2002; Chondrogen Inc. (CA)			
FEATURES	Location/Qualifiers			
source	1..523			
	/mol type="unassigned DNA"			
	/db_xref="taxon:9606"			
 <b>ORIGIN</b>				
Query Match	100.0%;	Score 327;	DB 6;	Length 523;
Best Local Similarity	100.0%;	Pred. No. 3..6e-184;	Indels 0;	Gaps 0;
Matches 327;	Conservative 0;	Mismatches 0;		
Qy	1 ATGGGGCACCGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Qy	Qy	Qy
Db	19 ATGGGGCACCGATGGATGCCAGGGACCAACAGGGCGGGCAAGAAC	Db	Db	Db



REFERENCE	2 (bases 1 to 535) Collins,J.B., Wright,C.L., Edwards,C.A., Davis,M.P., Grinham,J.A., Huckle,C.G., Gowd,B., Mallia,M., Mokrab,Y., Huckle,E.J., Beare,D.M., and Dunham,I.	SOURCE ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
TITLE	Direct Submission	1 (bases 1 to 534)
JOURNAL	Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk	REFERENCE AUTHORS Straubhaar,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Schuler,G.D., Klauser,R.D., Collins,F.S., Wagner,L., Schaefer,C.F., Bhat,N.K., Altschul,S.F., Zeeberg,B., Buetow,K.H., Shemesh,C.M., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Balonado,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loqueland,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEvlan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villaion,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Heitton,B., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.C., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J.J., Myers,R.M., Butterfield,Y.S., Krizynski,M.I., Skalska,U., Smilus,D.E., Schnurch,A., Schein,J.E., Jones,S.J. and Marrs,M.A.
COMMENT	Homo Sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see <a href="http://www.sanger.ac.uk/HSP/Chr22/">http://www.sanger.ac.uk/HSP/Chr22/</a> .	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) JOURNAL PUBLMED 2 (bases 1 to 534)
FEATURES	Location/Qualifiers I. .535 (organism="Homo sapiens" (mol_type="mRNA" (db_xref="taxon:9606" (chromosome="22" (clone="pGEM RBX1" (lab_xref="JM109" I. .535 (gene="RBX1" I. .345 (gene="RBX1" (codon_start=1 (protein_id="CAQ30446_1" (db_xref="GI:47678651" (db_xref="GOA: P62877" (db_xref="InterPro:IPR001841" (db_xref="UniProt/Swiss-Prot:PS2877" (translation="MAAAMDYDVTPSCTNSGGAKKREVKKKNAVALWDDIVNDCAIQRNHNIDLCIEQANQASATSEBECTIAVQCVNHAFFHC1SWLKTQVCIDLNEWFOKYGH"	REFERENCE AUTHORS Straubhaar,R. TITLE JOURNAL NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgbpb3@mail.nih.gov">cgbpb3@mail.nih.gov</a> Tissue Procurement: ATCC CDNA Library Preparation: CLONTECH Laboratories, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Institute for Systems Biology <a href="http://www.systemsbiology.org">http://www.systemsbiology.org</a> contact: amadan@systemsbiology.org Anup Madan, Stephanie Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting Clones distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium (LILNL) at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22091459. Location/Qualifiers I. .534 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4055797" /tissue type="Brain, glioblastoma" /clone Lib="NIH MGC_57" /lab host="DH10B" /note="vector: pDNR-LIB" I. .554 /gene=RBX1" /note="synonyms": ROC1, BA554C12.1, MGC13357, MGC1481, RNFI75" /db_xref="GeneID:9978" /db_xref="MIM:603814" <1..349 /gene=RBX1" /codon_start=2 /product="RBX1 protein" /protein_id="AAH17370.2"
ORIGIN	Query Match Score 327; DB 8; Length 535; Best Local Similarity 100.0%; Pred. No. 3 6e-184; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gars 0;	FEATURES SOURCE 1. CGCTTTGACTGAAAGTGAAATTCGATAGCCCTCTGGCCCGGATATTGGTGTAT 120 79 CGCTTTGAAAGTGAAATTCGATAGCCCTCTGGCGATTTGGTTAT 138 Db 1 ATGGCCGACGGCATGGTGGATAACCCTGGAGGGCACCAACAGCGGGGGAAAGAG 60 19 ATGGCCGACGGCATGGTGGATAACCCTGGAGGGCACCAACAGCGGGGGAAAGAG 78 Qy 61 CGCTTTGACTGAAAGTGAAATTCGATAGCCCTCTGGCCCGGATATTGGTGTAT 120 Db 79 CGCTTTGAAAGTGAAATTCGATAGCCCTCTGGCGATTTGGTTAT 138 Qy 121 AACCTGGCCATCTGGGACCAATTGGATGATGTTGATAGATGTAAGTAAACAG 180 Db 139 AACCTGGCCATCTGGGACCAATTGGATGATGTTGATAGATGTAAGTAAACAG 198 Qy 181 GGTCCTGGACTTCAAGAAGTGTACTGGCATGGAGTCCTAACATTGGCTTAC 240 Db 199 GGTCCTGGACTTCAAGAAGTGTACTGGCATGGAGTCCTAACATTGGCTTAC 258 Qy 241 TTCCACTGATCTCTGCCTGCAAAACAGGAGGGTGTCCATTGGGACAACAGAG 300 Db 259 TTCCACTGATCTCTGCCTGCAAAACAGGAGGGTGTCCATTGGGACAACAGAG 318 Qy 301 TGGGATTCAAAAGTAGTGGCACTAG 327 Db 319 TGGGATTCAAAAGTAGTGGCACTAG 345 gene RESULT 16 BC017370 LOCUS BC017370 mRNA (cDNA clone IMAGE:4065797), partial DEFINITION Homo sapiens ring-box 1, mRNA (cDNA clone IMAGE:4065797), partial cDNA ACCESSION BC017370 VERSION GI:16924201 KEYWORDS

/db\_xref="GI:32425477"  
 /db\_xref="GeneID:9378"  
 /db\_xref="MTM:603814"  
 /translation="GRPCYSKMAAMDVDTPSCTNSGAKRKPEVKKKNAVALWANDI  
 VDNCAICRNHMDLCIEQANQASATSEETVAVGVNHAFFHCTISRWLKRTRQVCP  
 LDNREWEFORYGH"  
**misc\_feature**  
 80. 346  
 /gene="APC11"; Region: CCG5194, APC11, Component of SCF  
 ubiquitin ligase and anaphase-promoting complex  
 [posttranslational modification, protein turnover,  
 chaperones / Cell division and chromosome partitioning]  
 /db\_xref="CDD:COG5194"

**ORIGIN**

Query Match	100.0%	Score 327; DB 8; Length 554;	Db	Db
Best Local Similarity	100.0%	Pred. No. 3.6e-180;	Qy	Qy
Matches	327	Mismatches 0; Indels 0; Gaps 0;	Db	Db
Qy	1 ATGGCCGAGGGATGTGGATACCCGAGGGACCAACAGGGCGGGAAAGAG 60	Qy	188 CTACTTCAGAGAGGTGACTGTGGATGCCATTGGACATTTGCTTCACTCCACT 247	
Db	23 ATGGCCGAGGGATGTGGATACCCGAGGGACCAACAGGGCGGGAAAGAG 82	Db	181 CTACTTCAGAGAGGTGACTGTGGATGCCATTGGACATTTGCTTCACTCCACT 240	
Qy	61 CGCTTGAACTGAAAAAGTGAATGCAAGTGCATGCCCTCTGGGATATTGGCTGGAT 120	RESULT 18	188 CTACTTCAGAGAGGTGACTGTGGATGCCATTGGACATTTGCTTCACTCCACT 247	
Db	83 CGCTTGAACTGAAAAAGTGAATGCAAGTGCATGCCCTCTGGGATATTGGCTGGAT 142	LOCUS	HUMY060A05	
Qy	121 AACCTGCCCCATCTGAGGAACCACATTATGATCTTGCATAGATCTAACGCTAACAG 180	DEFINITION	Homo sapiens full length insert cDNA clone Y060A05.	
Db	143 AACCTGCCCCATCTGAGGAACCACATTATGATCTTGCATAGATCTAACGCTAACAG 202	ACCESSION	AF085906	
Qy	181 GCGTCGGCTACTTCAGAGGTGTACTGTGGCATGGAGTCGTAAACCATGCTTTCAC 240	VERSION	AF085906.1	
Db	203 GCGTCGGCTACTTCAGAGGTGTACTGTGGCATGGAGTCGTAAACCATGCTTTCAC 262	KEYWORDS	FLJ_13246	
Qy	241 TTCCACTGCATCTCTGCTGGCTCAAACACGACAGGTGTCCATTGGACAACAGAGAG 300	SOURCE	Homo sapiens (human)	
Db	263 TTCCACTGCATCTCTGCTGGCTCAAACACGACAGGTGTCCATTGGACAACAGAGAG 322	ORGANISM	Homo sapiens	
Qy	301 TCGGAATTCAAAAAATGTTGGCACTTAG 327	REFERENCE	1 (bases 1 to 497) Woessner,J., Tan,F.P., Marra,M., Kucaba,T., Yandell,M., Martin,J., Marth,G., Bowles,L., Wylie,T., Bowers,Y., Stepioe,M., Thising,B., Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B., Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R., Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behmeyer,K., Hillier,L., Wilson,R. and Waterston,R.	
Db	323 TCGGAATTCAAAAAATGTTGGCACTAG 349	AUTHORS	Thiesen,H.J. and Lorenz,P.	

RESULT 17

CO832496	C0832496	503 bp DNA	linear	PAT 29-JUL-2004
DEFINITION	Sequence 160 from Patent WO2004058972.			JOURNAL
ACCESSION	C0832496			COMMENT
VERSION	C0832496.1			
KEYWORDS				SUBMITTED BY:
SOURCE	Homo sapiens (human)			Genome Sequencing Center
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.			Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA <a href="http://genome.wustl.edu/gsc">http://genome.wustl.edu/gsc</a> mailto:est@watson.wustl.edu
REFERENCE	1.			
AUTHORS	Thiesen,H.J. and Lorenz,P.			
TITLE	Human autoantgens and use thereof			
JOURNAL	Patent: WO 2004058972-A 160 15-JUL-2004;			
FEATURES	Thiesen, Hans-Juergen (DE); Lorenz, Peter (DE)			
Source	1..503			
	/organism="Homo sapiens"			
	/mol_type="unassigned DNA"			

**ORIGIN**

Query Match	97.9%	Score 320; DB 6; Length 503;	Db	Db
Best Local Similarity	100.0%	Pred. No. 5.7e-180;	Qy	Qy
Matches	320	Mismatches 0; Indels 0; Gaps 0;	Db	Db
Qy	8 CAGGCATGGATGTGGATACCCGAGGGCACCAACAGGGCGGGCAAGAGGCTTRG 67	RESULT 17	8 CAGGCATGGATGTGGATACCCGAGGGCACCAACAGGGCGGGCAAGAGGCTTRG 67	

FEATURES	source	FEATURES	source	FEATURES	source
ZK287.5	The location of this clone is unknown.	MILLIENIUM PREDICTIVE MEDICINE, INC. (US)	Location/Qualifiers	MILLIENIUM PREDICTIVE MEDICINE, INC. (US)	Location/Qualifiers
1. 497	/organism="Homo sapiens"	1. .4176	/organism="Homo sapiens"	1. .4176	/organism="Homo sapiens"
	/mol_type="mRNA"		/mol_type="unassigned DNA"		/mol_type="unassigned DNA"
	/db_xref="taxon:9606"		/db_xref="caxon:9606"		
misc_feature	/clone="IMAGE:20144" /clone lib="Soares_fetal_liver_spleen_1NPLS"	Query Match 94.2%; Score 308; DB 6; Length 4476;	Query Match 94.2%; Score 308; DB 6; Length 4476;	Query Match 94.2%; Score 308; DB 6; Length 4476;	Query Match 94.2%; Score 308; DB 6; Length 4476;
misc_feature	3. 305 /note="similar to Caenorhabditis elegans protein Z70757 (PID:gi1262999)"	Best Local Similarity 100.0%; Pred. No. 9.9e-173; Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 9.9e-173; Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 9.9e-173; Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 9.9e-173; Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
misc_feature	18. 284 /note="similar to Caenorhabditis elegans protein U80449 (PID:gi1707066)"	Db 1014 GCACCGATGCGATGGATACCCGAGGCCACAAACGGGGGAAGAGCGCTTT 66			
misc_feature	36. 302 /note="similar to Saccharomyces cerevisiae protein S66830 (PID:gi2132017)"	Qy 7 GCACCGATGCGATGGATACCCGAGGCCACAAACGGGGGAAGAGCGCTTT 66			
misc_feature	42. 302 /note="similar to Schizosaccharomyces pombe protein Z98977 (PID:gi2388937)"	Db 954 GAAGTGAAGTGAATGGAACTGAGTCAGTGCCCTGGGATATTGTGGTGTAAACTGT 895			
misc_feature	51. 284 /note="similar to Caenorhabditis elegans protein Z46242 (PID:gi559430)"	Qy 127 GCCATCTGCAGAACCAATTATGGATCTTGCATAGATGCTAAGGTAAACCAGCGCTTC 186			
ORIGIN		Db 894 GCCATCTGCAGAACCAATTATGGATCTTGCATAGATGCTAAGGTAAACCAGCGCTTC 835			
Query Match 94.2%; Score 308; DB 8; Length 497;	Db 187 GCTTACTTCAAGAAGGTGACTGTGCTATGGGAGCTGTAACTGTGCTTCACTTCCAC 246				
Best Local Similarity 100.0%; Pred. No. 9.1e-173; Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db 834 GCTTCTTCAGAAGGTGACTGTGCTATGGGAGCTGTAACTGTGCTTCACTTCCAC 775				
Qy 20 TGGATACCCGAGCCACCAACAGGGCGGGATATTGGTGTAAACTGTGCTATCTGCAGGA 79	Db 247 TGCACTCTCGCTGGCTCAAACACGACAGGTGTCCATTGGACAAGAGACTGGAA 306				
Db 1 TGGATACCCGAGCCACCAACAGGGCGGGATATTGGTGTAAACTGTGCTATCTGCAGGA 79	Db 774 TGCACTCTCGCTGGCTCAAACACGACAGGTGTCCATTGGACAAGAGACTGGAA 715				
Qy 20 TGGATACCCGAGCCACCAACAGGGCGGGATATTGGTGTAAACTGTGCTATCTGCAGGA 79	Db 307 TTCCAAA 314				
Db 61 GGATGCAAGTAGCCCTCTGGCCCTGGCCCTGGGATATTGGTGTAAACTGTGCTATCTGCAGGA 120	Db 714 TTCCAAA 707				
RESULT 20	HSTEST/C	HSTEST/C	HSTEST/C	HSTEST/C	HSTEST/C
Qy 140 ACCACATATGGATCTGGATAGATGTAAGGTAACTGGTACGTCACTCGAG 199	LOCUS H. sapiens mRNA for testican.				
Db 121 ACCACATATGGATCTGGATAGATGTAAGGTAACTGGTACGTCACTCGAG 180	DEFINITION X73608				
Qy 200 AGTGTACTGTCGGCATGGGAGTCTCAACCATGGTTCACCTCCTCGCT 259	VERSION X73608.1				
Db 181 AGTGTACTGTCGGCATGGGAGTCTCAACCATGGTTCACCTCCTCGCT 240	KEYWORDS testican.				
Qy 260 GGCTCAAACAGCACAGGCTGTCATGGACAAACAGAGGTGGGAATTCACAAAGATG 319	SOURCE Homo sapiens (human)				
Db 241 GGCTCAAACAGCACAGGCTGTCATGGACAAACAGAGGTGGGAATTCACAAAGATG 300	ORGANISM Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	ORGANISM Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	ORGANISM Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	ORGANISM Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	ORGANISM Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
Qy 320 GGCACTAG 327	REFERENCE Alliel, P.M., Perin, J.-P., Jolles, P. and Bonnet, F.J.	REFERENCE Alliel, P.M., Perin, J.-P., Jolles, P. and Bonnet, F.J.	REFERENCE Alliel, P.M., Perin, J.-P., Jolles, P. and Bonnet, F.J.	REFERENCE Alliel, P.M., Perin, J.-P., Jolles, P. and Bonnet, F.J.	REFERENCE Alliel, P.M., Perin, J.-P., Jolles, P. and Bonnet, F.J.
Db 301 GGCACTAG 308	TITLE Testican, a multidomain testicular proteoglycan resembling modulators of cell social behaviour	TITLE Testican, a multidomain testicular proteoglycan resembling modulators of cell social behaviour	TITLE Testican, a multidomain testicular proteoglycan resembling modulators of cell social behaviour	TITLE Testican, a multidomain testicular proteoglycan resembling modulators of cell social behaviour	TITLE Testican, a multidomain testicular proteoglycan resembling modulators of cell social behaviour
RESULT 19	JOURNAL Eur. J. Biochem. 214 (1), 347-350 (1993)	JOURNAL Eur. J. Biochem. 214 (1), 347-350 (1993)	JOURNAL Eur. J. Biochem. 214 (1), 347-350 (1993)	JOURNAL Eur. J. Biochem. 214 (1), 347-350 (1993)	JOURNAL Eur. J. Biochem. 214 (1), 347-350 (1993)
CQ43737	PUBMED 8389704				
LOCUS PAT 30-JAN-2004	FEATURES Source				
DEFINITION Sequence 25604 from Patent WO160860.					
ACCESSION C0493737					
VERSION C0493737					
KEYWORDS					
SOURCE Homo sapiens (human)					
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE 1 Schlegel, R.; Endge, W.O. and Monahan, J.B.					
AUTHORS Genes differentially expressed in human prostate cancer and their use					
TITLE Patent: WO 0160860-A 25604 23-AUG-2001;					
JOURNAL					

EDANRVIKPTSSNTAQQGREDTSILPICKDSIGHMENKLDMNYDILLDBSEINAIVLDK YPCIKPLNNSCDSFRDGKLSQCPQKCNMRCQWVCDYKGNEBLASRKOGAVSCBEEQIOTSKDFSGGSV VLDDLEYERELGPDKDEKGSLRVHTRAVTEDDEDDEDDKEDEVYIW"	ORIGIN	Query Match Score 84.1%; Score 275; DB 8; Length 306; Pred. No. 5.7e-153; N mismatches 0; Indels 0; Gaps 0; Best Local Similarity 100.0%;保守性匹配 275; 相似度 100.0%; 保守性匹配 0; 不匹配 0; 缺口 0;
Query Match Score 90.5%; Score 296; DB 8; Length 3484; Best Local Similarity 100.0%; Pred. No. 1.6e-165; N mismatches 0; Indels 0; Gaps 0; Matches 296; 保守性匹配 0; 不匹配 0; 缺口 0;	Qy	53 GCAAGAAAGCCCTTGAAGTCATAAGTGGCATAGGCCCTTGGGATATTG 112 Db 16 GCAAGAAAGCCCTTGAAGTCATAAGTGGCATAGGCCCTTGGGATATTG 75
Qy 7 GCAGCGATGGATGTGGATAACCCGAGGGCACCAAGAGCAGCGCGGGCAGAAGGGCTT 66 Db 296 GCAGCGATGGATGTGGATAACCCGAGGGCACCAAGAGCAGCGCGGGCAGAAGGGCTT 237	Qy	113 TGGTGATAACTGTGCCATCTGAGAACACATTGGATCTTGATAGAAATGTCAG 172 Db 76 TGGTGATAACTGTGCCATCTGAGAACACATTGGATCTTGATAGAAATGTCAG 135
Qy 67 GAACTGAAAAGTGGATGTGGATGTGGATATTGGTTGATACTGT 126 Db 236 GAACTGAAAAGTGGATGTGGATGTGGATATTGGTTGATACTGT 177	Qy	173 CTAACAGGGTCCCTACTTCAGAAAGTGTACTGTCGATGGGAGTCGTGAAACCATG 232 Db 136 CTAACAGGGTCCCTACTTCAGAAAGTGTACTGTCGATGGGAGTCGTGAAACCATG 195
Qy 127 GCCATCTGCAGAACCAATTATGGATCTTGATAGAAATGCAAGCTAACCGCCGCC 186 Db 176 GCCATCTGCAGAACCAATTATGGATCTTGATAGAAATGCAAGCTAACCGCCGCC 117	Qy	233 CTTTCACTTCACCTGCACTCTGCTGGTCAAACACAGACAGCTGGCCATGGACA 292 Db 196 CTTTCACTTCACCTGCACTCTGCTGGTCAAACACAGACAGCTGGCCATGGACA 255
Qy 187 GCTACTCTAGAGAGTGACTGTGGATGGGAGCTGTACCATGCTTCACTTCAC 246 Db 116 GCTACTCTAGAGAGTGACTGTGGATGGGAGCTGTACCATGCTTCACTTCAC 57	Qy	293 ACAGAGAGTGGATTCCAAAAGTAGGGACTAG 327 Db 256 ACAGAGAGTGGATTCCAAAAGTAGGGACTAG 290
Qy 247 TGCATCTCTCGCTGGTCAAAACACGACAGGTGTGTCATGGACACAGAGATG 302 Db 56 TGCATCTCTCGCTGGTCAAAACACGACAGGTGTGTCATGGACACAGAGATG 1	RESULT 22	CQ702730 468 bp DNA linear PAT 03-FEB-2004
LOCUS CQ702730 Sequence 47656 from Patent WO20070737.	LOCUS	CQ702730
DEFINITION C0702730 Version 47656	DEFINITION	C0702730
ACCESSION C0702730 GI:42263499	ACCESSION	C0702730
VERSION C0702730.1	VERSION	C0702730.1
KEYWORDS Homo sapiens (human)	KEYWORDS	Homo sapiens
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1	REFERENCE	Liew, C.C., Marshall, W.E. and Zhang, H.
AUTHORS Liaw, C.C., Marshall, W.E. and Zhang, H.	AUTHORS	Compositions and methods relating to osteoarthritis
TITLE Title	JOURNAL	WO 02070737-A 12-SEP-2002;
VERSION	FEATURES	Chondrogen Inc. (CA)
SOURCE Source	FEATURES	Location /Qualifiers
1	1	1 - 468
ORGANISM Homo sapiens	ORGANISM	/mol_type="Homo sapiens"
DEFINITION Homo sapiens ZYP protein mRNA, partial cds.	DEFINITION	/mol_type="unassigned DNA"
ACCESSION AY099360	ACCESSION	/db_xref="taxon:3606"
VERSION AY099360.1	VERSION	
SOURCE Homo sapiens (human)	SOURCE	
REFERENCE 1	REFERENCE	
AUTHORS Perin, J.-P., Seddiki, N., Charbonnier, F., Goudou, D., Belkadi, L., Rieger, F. and Alliel, P.M.	AUTHORS	
TITLE Genomic organization and expression of the ubiquitin-proteasome complex-associated protein Rbx1/Hrt1	TITLE	
JOURNAL Cell. Mol. Biol. (Noisy-le-grand) 45 (8), 1131-1137 (1999)	JOURNAL	
PUBMED 10643962	PUBMED	
REFERENCE 2 (bases 1 to 306)	REFERENCE	
AUThORS Alliel, P.M., Seddiki, N., Belkadi, L., Lecoeur, L. and Perin, J.P.	AUThORS	
TITLE Direct Submission	TITLE	
JOURNAL Submitted (23-APR-2002) U488, INSERM, 80, rue du General Leclerc, Le Kremlin-Bicetre 94270, France	JOURNAL	
FEATURES Source	FEATURES	
1..306	1..306	
/organism="Homo sapiens"	/organism="Homo sapiens"	
/mol_type="mRNA"	/mol_type="mRNA"	
/db_xref="taxon:9606"	/db_xref="taxon:9606"	
/clone="yp3"	/clone="yp3"	
/sex="male"	/sex="male"	
/tissue_type="whole brain"	/tissue_type="whole brain"	
/dev_stage="26-week fetus"	/dev_stage="26-week fetus"	
<1..290	<1..290	
CDS	CDS	
/product_start=3	/product_start=3	
/product_end=1	/product_end=1	
/protein_id="PAM21718_1"	/protein_id="PAM21718_1"	
/db_xref="GI:2050205"	/db_xref="GI:2050205"	
/translation="NSGASKRFEVKWWNAVALWAVDIVDNCIAICRNHIMLICIEQ ANQASATSECTVAYGVCNHAFFHC1SRWLKTRQVCPIDNNEWFQKYGH"	/translation="NSGASKRFEVKWWNAVALWAVDIVDNCIAICRNHIMLICIEQ ANQASATSECTVAYGVCNHAFFHC1SRWLKTRQVCPIDNNEWFQKYGH"	



**RESULT 26**  
**AR651451 AR651451** Query Match Score 249; DB 6; Length 3208;  
**LOCUS Sequence 27 from patent US 6881563.** Best Local Similarity 100.0%; Pred. No. 2.8e-137;  
**DEFINITION** Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**ACCESSION AR651451**  
**VERSION AR651451.1 GI:62795924**  
**KEYWORDS Unknown.**  
**SOURCE Unknown.**  
**ORGANISM Unclassified.**

**REFERENCE 1 (bases 1 to 3208)**  
**AUTHORS Donoho, G., Scoville, J., Turner, C.A. Jr., Friedrich, G., Abuin, A.,**  
**JOURNAL Human proteases and polynucleotides encoding the same**  
**TITLE Patent: US 6881563-A 27-19-APR-2005;**  
**FEATURES Lexicon Genomics Incorporated; The Woodlands, TX**  
**Source**  
**1. 3208 /organism="unknown"**

**ORIGIN**

Query Match Score 249; DB 6; Length 3208;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;  
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 79 TGGATGCACTGGCCCTCTGGCATATTGGCTGATAACTGGCCATCTGCAGC 138  
**Db** 2776 TGGATGCACTGGCCCTCTGGCATATTGGCTGATAACTGGCCATCTGCAGC 2835

**Qy** 139 AACACATATTGGATTTGGATCTTCATAGAAATGTCAAGTAACAGGCTCGCTACTCGA 198  
**Db** 2836 AACACATATTGGATCTTCATAGAAATGTCAAGTAACAGGCTCGCTACTCGA 2895

**Qy** 199 GAGTGTACTGTCGATGGGAGTCGTAACTGCTTTCACITCCACNGCATCTCGC 258  
**Db** 2896 GAGTGTACTGTCGATGGGAGTCGTAACTGCTTTCACITCCACNGCATCTCGC 2955

**Qy** 259 TGGCTCAAAACAGCACAGGCTGGCTCATTCGACAAAGAGCTGGAAATTCCA 318  
**Db** 2956 TGGCTCAAAACAGCACAGGCTGGCTCATTCGACAAAGAGCTGGAAATTCCA 3015

**Qy** 319 GGGCACTAG 327  
**Db** 3016 GGGCACTAG 3024

**RESULT 27**  
**AX212267 AX212267** Query Match Score 207; DB 6; Length 430;  
**LOCUS Sequence 27 from Patent WO0159134.** Best Local Similarity 99.7%; Pred. No. 3.8e-112;  
**DEFINITION** Matches 327; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
**ACCESSION AX212267**  
**VERSION AX212267.1 GI:15524031**  
**KEYWORDS**  
**SOURCE Homo sapiens (human)**  
**ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;**  
**Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;**  
**Hominidae; Homo.**  
**REFERENCE 1**  
**AUTHORS Donoho, G., Scoville, J., Turner, C.A., Friedrich, G.B., Abuin, A.,**  
**Zambrowicz, B., and Sands, A.T.**  
**JOURNAL Human proteases and polynucleotides encoding the same**  
**TITLE Patent: WO 0159134-A 27-16-AUG-2001;**  
**FEATURES Lexicon Genomics Incorporated (US)**  
**Source**  
**1. 3208 /organism="Homo sapiens"**  
**/mol\_type="unassigned DNA"**  
**Db \_xref="taxon:9606"**

**ORIGIN**

Query Match Score 207; DB 6; Length 430;  
 Best Local Similarity 99.7%; Pred. No. 3.8e-112;  
 Matches 327; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

**Qy** 1 ATGGGGCACCCGATGGATGGATGGATACCCGAGGCCACACGGCCGGCCAGAAG 60  
**Db** 21 ATGGGGCACCCGATGGATGGATGGATACCCGAGGCCACACGGCCGGCCAGAAG 80

**Qy** 61 CGGTTGAAGTAAAAAGTGGAAATTGGCTGAGGTTGATTTGGCTTGAT 120  
**Db** 81 CGGTTGAAGTAAAAAGTGGAAATTGGCTGAGGTTGATTTGGCTTGAT 140

**Qy** 121 AACGTGCCATCTCGGACCAATTGGATTTGGATAGATGTCAGCTTCAAGCTTCCA 179  
**Db** 141 AACGTGCCATCTCGGACCAATTGGATTTGGATAGATGTCAGCTTCCAAGCTTCCA 200

**Qy** 180 GGCTCCGCTACTTCGAGAGGTGTTGCTGCTGGAGTCGTAACTGGCTTCCA 239  
**Db** 201 GGCTCCGCTACTTCGAGAGGTGTTGCTGCTGGAGTCGTAACTGGCTTCCA 260

**Qy** 240 CTTCACACTGCACTCTCGCTGGCTCAAACACGACAGGTGTCATTGGACACAGAGA 299  
**Db** 261 CTTCACACTGCACTCTCGCTGGCTCAAACACGACAGGTGTCATTGGACACAGAGA 320

**ORIGIN**

			1. .300
Qy	300 GTCGGAAATTCCAAAAGTATGGGCACTAG 327	source	/organism="Homo sapiens"
Db	321 GTGGGAATTCCAAAAGTATGGGCACTAG 348		/mol_type="unassigned DNA" /db_xref="taxon:9606"
RESULT 29		ORIGIN	
CQ705678	CQ705678 Sequence 50604 from Patent WO20070737.	Query Match	52.9%; Score 173; DB 6; Length 300;
DEFINITION		Best Local Similarity 100.0%; Pred. No. 9.7e-92;	
ACCESSION	CQ705678	Mismatches 0; Indels 0; Gaps 0;	
VERSION	CQ705678.1 GI: 42266447	Matches 1/3; Conservative 0;	
KEYWORDS		Query 88 GTAGGCCCTCTGGGCCTGGGATATTCGGGTGATAACTGTGCGGAAACCACATT 147	
SOURCE	Homo sapiens (human)	Db 41 GTAGGCCCTCTGGGCCTGGGATATTCGGGTGATAACTGTGCGGAAACCACATT 100	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bacteria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	Query 148 ATGGATCTTTGATAGAATGTCAGAACTAACGGGTCGGTACTCTCAGAGTGACT 207	
REFERENCE	1. Liew,C.C., Marshall,W.E. and Zhang,H.	Db 101 ATGGATCTTTGATAGAATGTCAGAACTAACGGGTCGGTACTCTCAGAGTGACT 160	
AUTHORS		208 GTCGCATGGGAGTGTAAACCATGCTTCACTTCACACTGCACTCTCGCTG 260	
TITLE	Compositions and methods relating to osteoarthritis	Db 161 GTCGCATGGGAGTGTAAACCATGCTTCACTTCACACTGCACTCTCGCTG 213	
JOURNAL	Patent: WO 02070737-A 50604 12-SEP-2002;		
FEATURES source	Chondrogenic Inc. (CA) Location/Qualifiers	RESULT 31	
	1. .475 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	BD030041 LOCUS BD030041 402 bp DNA linear PAT 27-AUG-2002	
ORIGIN		DEFINITION Sequence tag and encoded human protein.	
		ACCESSION BD030041	
		VERSION BD030041.1 GI:22571783	
		KEYWORDS JP 2001269102-A/6287.	
		ORGANISM Homo sapiens (human)	
		Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Homo.	
		REFERENCE (bases 1 to 402) 1. Edwards,J.B.D.M., Ducleir,B. and Jordaan,J.Y.	
		AUTHORS Edwards,J.B.D.M., Ducleir,B. and Jordaan,J.Y.	
		TITLE Sequence tag and encoded human protein	
		JOURNAL Patent: JP 2001269102-A 6287 02-OCT-2001; GENSET	
		COMMENT OS Homo sapiens (human)	
		PN JP 2001269102-A/6287	
		PD 02-OCT-2001	
Query	12 GATGGATCTGGATACCCGAGGGCACCAACACGGCCGGGAAAGANGGCCTTTGAGT 71	Db 2 GATGGATCTGGATACCCGAGGGCACCAACACGGCCGGGAAAGAGGCGCTTTGAGT 61	PP 24-FEB-2000 JP 2000111873
Db	132 CTGAGGAAACACATTATGGATCTTGGATAGAATGTCAGTAACCGGGCTCGCTAC 191	Db 122 CTGAGGAAACACATTATGGATCTTGGATAGAATGTCAGTAACCGGGCTCGCTAC 181	PR 26-FEB-1999 US 60/122487
Query	72 GAAAAATGTTGAAATGCACTGGATGGCCCTCTGGCCTGGATATTGGTTGATACTGTGCAT 131	Db 192 TTCAAGAAGTGTACTGCTGCAACCATGCTGCTTCACTTCACGTGAT 251	PI JEBAN BAPTISTE DONAS MLINE EDWARDS, EIMERIC DUCLAIR, JEAN YVES JORDAN PC C12N5/10, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10, C12P21/08, C12Q1/68//G06F17/30, C12N5/00, C12N5/00, PC G06F15/40
Db	62 GAAAATGTTGAAATGCACTGGATGGCCCTCTGGCCTGGATATTGGTTGATACTGTGCAT 121	CC CC	CC CC
Query	132 CTGAGGAAACACATTATGGATCTTGGATAGAATGTCAGTAACCGGGCTCGCTAC 191	Db 182 TTCAAGAAGTGTACTGCTGCAACCATGCTGCTTCACTTCACGTGAT 241	FH FH Key Location/Qualifiers
Db	122 CTGAGGAAACACATTATGGATCTTGGATAGAATGTCAGTAACCGGGCTCGCTAC 181	Db 252 CTCTCGCTG 260	1. .402 Location/Qualifiers
Query	192 TTCAAGAAGTGTACTGCTGCAACCATGCTGCTTCACTTCACGTGAT 251	Db 242 CTCTCGCTG 250	1. .402 Location/Qualifiers
Db	182 TTCAAGAAGTGTACTGCTGCAACCATGCTGCTTCACTTCACGTGAT 241		
Query	252 CTCTCGCTG 260		
Db	242 CTCTCGCTG 250		
RESULT 30		FEATURES source	
CQ703590	CQ703590 Sequence 48516 from Patent WO20070737.	Query Match	52.0%; Score 170; DB 6; Length 402;
DEFINITION		Best Local Similarity 100.0%; Pred. No. 6.2e-90;	
ACCESSION	CQ703590	Mismatches 0; Indels 0; Gaps 0;	
VERSION	CQ703590.1 GI: 42264359	Matches 170; Conservative 0;	
KEYWORDS	Homo sapiens (human)	Query 158 GCATAGAAATGTCAAAGCTAACCGGGCTCGGTACTCTCAGAAAGTGTACTGTGCACTGG 217	
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bacteria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	Db 106 GCATAGAAATGTCAAAGCTAACCGGGCTCGGTACTCTCAGAAAGTGTACTGTGCACTGG 165	
ORGANISM	1. Liew,C.C., Marshall,W.E. and Zhang,H.	Query 218 GAGTGTGTAACCATGCTTCACTTCACGCACTGCTGCTGCTGCACTGG 277	
REFERENCE	Compositions and methods relating to osteoarthritis	Db 166 GAGTGTGTAACCATGCTTCACTTCACGCACTGCTGCTGCACTGG 225	
AUTHORS	Patent: WO 02070737-A 48516 12-SEP-2002;		
TITLE	Chondrogenic Inc. (CA)		
JOURNAL	Location/Qualifiers		
FEATURES			





Matches	148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES	Location/Qualifiers
Qy	96 CTGGGCTTGGATATTGGTGTATACTGTCATCTGAGAACCATATTGGATCT 155	/organism="Homo sapiens"	1. .135
Db	91 CTGGCCTGGATATTCTGTGATAACTGTCATCTGAGAACCATATTGGATCT 150	/mol_type="unassigned DNA"	/db_xref="taxon:9606"
		ORIGIN	
		Query Match	40.4%; Score 132; DB 6; Length 135;
		Best Local Similarity 100.0%; Pred. No. 3.9e-67;	Mismatches 0; Indels 0; Gaps 0;
		Matches 132; Conservative 0;	
Qy	156 TTGATAGAATGTCAGGCTCGTACPTCAAGAGGTGACTGTGATG 215	Qy	1 ATGGCCACCCGATGCGATACCCGAGCCACACGGCCGGCAAGAG 60
Db	151 TTGATAGAATGTCAGGCTCGTACPTCAAGAGGTGACTGTGATG 210	Db	4 ATGGCCACCCGATGCGATGCGATGCGACCAACAGGGCAAGAAG 63
Qy	216 CGGAGCTGTAACTGACCATGCTTCACTTCACITC 243	Qy	61 CGCTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120
Db	211 GGAGCTGTAACTGCTTCACTTCACITC 238	Db	64 CGCTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 123
		RESULT 39	
		LOCUS	CQ686479 450 bp DNA linear PAT 03-FEB-2004
		DEFINITION	Sequence 31405 From Patent WO20070737.
		VERSION	CQ686479 1 GI:42215585
		KEYWORDS	
		SOURCE	Homo sapiens (human)
		ORGANISM	Buaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Liew, C.C., Marshall,W.E. and Zhang,H.	AUTHORS	Liew, C.C., Marshall,W.E. and Zhang,H.
AUTHORS	Liew, C.C., Marshall,W.E. and Zhang,H.	TITLE	Compositions and methods relating to osteoarthritis
TITLE	Composition and methods relating to osteoarthritis	JOURNAL	Patent: WO 02070737-A 53800 12-SEP-2002;
JOURNAL	Chondrogen Inc. (CA)	FEATURES	Accession CQ708874.1 GI:42269668
		source	Source Homo sapiens (human)
		FEATURES	Organism Homo sapiens
		source	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
		ORIGIN	
		Query Match	43.1%; Score 141; DB 6; Length 450;
		Best Local Similarity 100.0%; Pred. No. 1.6e-72;	Mismatches 0; Indels 0; Gaps 0;
		Matches 141; Conservative 0; Mismatches 0;	
Qy	158 SCATAGAATGCAAGCTAACAGGCCTCGCTACTTCAGAAAGGTGACTGTGCAATGGG 217	Qy	158 GCATAGAATGTCAGCTAACAGGCCTCGCTACTTCAGAAAGGTGACTGTGCAATGGG 217
Db	109 SCATAGAATGCAAGCTAACAGGCCTCGCTACTTCAGAAAGGTGACTGTGCAATGGG 168	Db	82 GCATAGAATGTCAGCTAACAGGCCTCGCTACTTCAGAAAGGTGACTGTGCAATGGG 141
Qy	218 GAGTCCTGACATGCTTTCACTTCACTGATCTCGCTCAAACAGGAGG 277	Qy	218 GAGTCCTGACATGCTTTCACTTCACTGATCTCGCTCAAACAGGAGG 277
Db	169 GAGTCCTGACATGCTTTCACTTCACTGATCTCGCTCAAACAGGAGG 228	Db	142 GAGTCCTGACATGCTTTCACTTCACTGATCTCGCTCAAACAGGAGG 201
Qy	278 TGTGTCATGACAAAGAG 298	Qy	278 TGTTGCAATGACAAAGAG 281
Db	229 TGTGTCATGACAAAGAG 249	Db	202 TGTTGCAATGACAAAGAG 205
		RESULT 40	
		LOCUS	CQ668705 135 bp DNA linear PAT 03-FEB-2004
		DEFINITION	Sequence 13631 From Patent WO200737.
		VERSION	CQ668705 1 GI:42157083
		KEYWORDS	
		SOURCE	Homo sapiens (human)
		ORGANISM	Buaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Liew, C.C., Marshall,W.E. and Zhang,H.	AUTHORS	Liew, C.C., Marshall,W.E. and Zhang,H.
AUTHORS	Compositions and methods relating to osteoarthritis	TITLE	Patent: WO 02070737-A 13631 12-SEP-2002;
TITLE	Chondrogen Inc. (CA)	JOURNAL	
JOURNAL		FEATURES	Accession CQ688757
		source	Source Homo sapiens (human)
		FEATURES	Organism Homo sapiens
		ORIGIN	
		Query Match	37.9%; Score 124; DB 6; Length 325;
		Best Local Similarity 100.0%; Pred. No. 2.5e-62;	Mismatches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		Matches 124; Conservative 0;	
Qy	158 GCATAGAATGTCAGCTAACAGGCCTCGCTACTTCAGAAAGGTGACTGTGCAATGGG 217	Qy	158 GCATAGAATGTCAGCTAACAGGCCTCGCTACTTCAGAAAGGTGACTGTGCAATGGG 217
Db	82 GCATAGAATGTCAGCTAACAGGCCTCGCTACTTCAGAAAGGTGACTGTGCAATGGG 141	Db	142 GAGTCCTGACATGCTTTCACTTCACTGATCTCGCTCAAACAGGAGG 201
Qy	218 GAGTCCTGACATGCTTTCACTTCACTGATCTCGCTCAAACAGGAGG 277	Qy	218 GAGTCCTGACATGCTTTCACTTCACTGATCTCGCTCAAACAGGAGG 277
Db	142 GAGTCCTGACATGCTTTCACTTCACTGATCTCGCTCAAACAGGAGG 201	Db	202 TGTTGCAATGACAAAGAG 205
		RESULT 42	
		LOCUS	CQ688757 363 bp DNA linear PAT 03-FEB-2004
		DEFINITION	Sequence 33683 From Patent WO200737.
		VERSION	CQ688757
		KEYWORDS	
		SOURCE	Homo sapiens (human)
		ORGANISM	Buaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Liew, C.C., Marshall,W.E. and Zhang,H.	AUTHORS	Liew, C.C., Marshall,W.E. and Zhang,H.
AUTHORS	Compositions and methods relating to osteoarthritis	TITLE	Patent: WO 02070737-A 13631 12-SEP-2002;
TITLE	Chondrogen Inc. (CA)	JOURNAL	
JOURNAL		FEATURES	Accession CQ688757
		source	Source Homo sapiens (human)
		FEATURES	Organism Homo sapiens
		ORIGIN	



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

## OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 15:18:35 ; Search time 659.377 Seconds

(without alignments)

4100.974 Million cell updates/sec

Title: US-09-541-462B-1

Perfect Score: 327

Sequence: 1 atggcgccatgtatggatgt.....tccaaaatgtggcactag 327

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters:

19587084

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summariesDatabase : Published Applications NA\_Main:/\*  
1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:/\*  
2: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:/\*  
3: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:/\*  
4: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:/\*  
5: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:/\*  
6: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:/\*  
7: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq:/\*  
8: /cgn2\_6/prodata/1/pubpna/US10D\_PUBCOMB.seq:/\*  
9: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq:/\*  
10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	433	7	US-10-242-525A-43377
2	327	100.0	433	7	US-10-085-783A-3377
3	327	100.0	453	7	US-10-242-535A-35025
4	327	100.0	453	7	US-10-085-783A-35025
5	327	100.0	467	7	US-10-242-535A-39933
6	327	100.0	467	7	US-10-085-783A-39933
7	327	100.0	471	7	US-10-242-535A-57254
8	327	100.0	471	7	US-10-085-783A-57254
9	327	100.0	472	7	US-10-242-535A-56068
10	327	100.0	472	7	US-10-085-783A-56068
11	327	100.0	508	8	US-10-913-937-3
12	327	100.0	523	7	US-10-242-535A-46292
13	327	100.0	523	7	US-10-085-783A-46292
14	325	99.4	476	3	US-09-918-905-17191
15	321.8	98.4	4543	5	US-10-198-846-11311
16	316	96.6	430	7	US-10-242-535A-54751
17	316	96.6	430	7	US-10-085-783A-54751
18	308.8	94.4	4476	8	US-10-357-930-25604
19	302.4	92.5	380	3	US-09-367-352-4677
20	301.2	92.1	5347	6	US-10-240-352-4677
21	296.8	90.8	3484	8	US-10-723-860-1383
22	296.8	90.8	3484	9	US-10-756-149-1387
23	296.8	90.8	5111	5	US-10-205-823-382

RESULT 1  
US-10-242-535A-43377  
; Sequence 43377, Application US/10242535A  
; Publication No. US20040013633A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY OR AGENT NAME:  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIORITY DATE: 2002-02-28  
; PRIORITY APPLICATION NUMBER: US 60/305,340  
; PRIORITY FILING DATE: 2001-07-13  
; PRIORITY APPLICATION NUMBER: US 60/275,017  
; PRIORITY FILING DATE: 2001-03-12  
; PRIORITY APPLICATION NUMBER: US 60/271,955  
; PRIORITY FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO: 43377  
; LENGTH: 433  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-242-535A-43377

Query Match 100.0%; Score 327; DB 7; Length 433;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; Query 1 ATGGCGCCAGGATGGATGCCAGCCACCAAGGGCGGGCAAGAG 60  
; Sequence 56068, A  
; Sequence 56068, A  
; Sequence 3, Appli  
; Sequence 39933, A  
; Sequence 39933, A  
; Sequence 57254, A  
; Sequence 56068, A  
; Sequence 56068, A  
; Sequence 54751, A  
; Sequence 46292, A  
; Sequence 17191, A  
; Sequence 11311, A  
; Sequence 54751, A  
; Sequence 25604, A  
; Sequence 4677, Ap  
; Sequence 99, Appli  
; Sequence 1383, Ap  
; Sequence 1357, Ap  
; Sequence 382, App  
; Sequence 5852, Ap  
; Sequence 5, Appli  
; Sequence 47656, A  
; Sequence 47656, A  
; Sequence 52747, A  
; Sequence 50604, A  
; Sequence 50604, A  
; Sequence 48516, A  
; Sequence 48516, A  
; Sequence 58211, A  
; Sequence 58211, A  
; Sequence 19847, A  
; Sequence 19847, A  
; Sequence 22649, A  
; Sequence 46883, A  
; Sequence 46883, A

## ALIGNMENTS

QY 241 TTCCCACTGGATCTCTGCTGGCTCAAACAGGACAGGTGTCATTGGACACAGAG 300  
 Db 260 TTCCCACTGGATCTCTGCTGGCTCAAACAGGACAGGTGTCATTGGACACAGAG 319

QY 301 TGGGAATTCAAAAGTATGGCACTAG 327  
 Db 320 TGGGAATTCAAAAGTATGGCACTAG 346

---

RESULT 2  
 US-10-085-783A-43377  
 ; Sequence 43377, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTOR: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-08  
 ; PRIORITY APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIORITY FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 43377  
 ; LENGTH: 433  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-242-535A-35025

Query Match Score 100.0%; Score 327; DB 7; Length 433;  
 Best Local Similarity 100.0%; Pred. No. 5.e-104;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGGGATGGATGGATGGATACCCCGAGGGCACCACGGGAGGGAAAGAG 60  
 Db 24 ATGGGGCGAGGGATGGATGGATGGATACCCGGAGGGCACCACGGGAGGGAAAGAG 83

Qy 61 CGCTTGTGAATGTAATAACTGGGAACTGGCATGGCTCTGGCCCTCTGGCTTGAT 120  
 Db 84 CGCTTGTGAATGTAATAACTGGGAACTGGCATGGCTCTGGCCCTCTGGCTTGAT 143

Qy 121 AACGTGCCATCTGGGACCAATTGGATGATGATGATGTTGGATGATGATGTAACCAG 180  
 Db 144 AACGTGCCATCTGGGACCAATTGGATGATGATGATGATGTTGGATGATGATGTAACCAG 203

Qy 181 GCCTCCGGTACTCTGGGAGGTACTGTGCATGGGAGTCTGTAACCATGGTTTCAC 240  
 Db 204 GCCTCCGGTACTCTGGGAGGTACTGTGCATGGGAGTCTGTAACCATGGTTTCAC 263

Qy 241 TTCACTGATCTCGCTGGCTCAAACACGACAGGTCTGACTGTGCATGGGAGTCTGTAACCATGGGAG 300  
 Db 264 TTCACTGATCTCGCTGGCTCAAACACGACAGGTCTGACTGTGCATGGGAGTCTGTAACCATGGGAG 323

Qy 301 TGGGAATTCCAAGAAGTGGCAATTGGATCTGGGATTAATGGTGTGAT 120  
 Db 324 TGGGAATTCCAAGAAGTGGCAATTGGATCTGGGATTAATGGTGTGAT 350

RESULT 4  
 US-10-085-783A-35025  
 ; Sequence 35025, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTOR: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIORITY APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIORITY FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SEQ ID NO: 35025  
 ; LENGTH: 453  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-085-783A-35025

Query Match Score 100.0%; Score 327; DB 7; Length 453;

Best Local Similarity 100.0%; Pred. No. 5.5e-104;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGCGATGGTGTGGTGTGGATAACCCGACGCCAACAGCCGAGAAG 60  
Db 24 ATGGCGAGCGATGGTGTGGTGTGGATAACCCGACGCCAACAGCCGAGAAG 83

Qy 61 CGTTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGATAATGGTTGAT 120  
Db 84 CGCTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGGATAATGGTTGAT 143

Qy 121 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTGATAGAAATTGTAACAG 180  
Db 144 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTGATAGAAATTGTAACAG 346

RESULT 6  
US-10-085-783A-39933  
; Sequence 39933, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; C.I.C.: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085783A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIORITY NUMBER: US 60/275,017  
; PRIORITY FILING DATE: 2001-03-12  
; PRIORITY APPLICATION NUMBER: US 60/271,955  
; PRIORITY FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 39933  
; LENGTH: 467  
; TYPE: DNA  
; ORGANISM: Human  
US-10-085-783A-39933

Query Match 100.0%; Score 327; DB 7; Length 467;  
Best Local Similarity 100.0%; Pred. No. 5.6e-104; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGCGATGGATGGATGGCATGCCAGGCCACCAAGGGCGGGCGGAGAAG 60  
Db 20 ATGGCGCAGCGATGGATGGCATGCCAGGCCACCAAGGGCGGGCGGAGAAG 79

Qy 61 CGTTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGATAATGGTTGAT 120  
Db 80 CGTTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGATAATGGTTGAT 139

Qy 121 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTGATAGAAATTGTAACAG 180  
Db 140 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTGATAGAAATTGTAACAG 199

Qy 181 CGCTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGATAATGGTTGAT 120  
Db 80 CGCTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGATAATGGTTGAT 139

RESULT 7  
US-10-242-535A-39933  
; Sequence 39933, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; C.I.C.: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 39933  
; LENGTH: 467  
; TYPE: DNA  
; ORGANISM: Human  
US-10-242-535A-39933

Query Match 100.0%; Score 327; DB 7; Length 467;  
Best Local Similarity 100.0%; Pred. No. 5.6e-104; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGCGATGGATGGGATACCCGAGGGGACCAACAGGGCGGGAGAAG 60  
Db 20 ATGGCGCAGCGATGGGATACCCGAGGGGACCAACAGGGCGGGAGAAG 79

Qy 61 CGTTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGATAATGGTTGAT 120  
Db 80 CGTTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGATAATGGTTGAT 139

Qy 121 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTGATAGAAATTGTAACAG 180  
Db 140 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTGATAGAAATTGTAACAG 199

Qy 181 CGCTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGATAATGGTTGAT 120  
Db 80 CGCTTGAAGTGAAGAAATGGGATAGCTGTAGCCCTGGGCTGGATAATGGTTGAT 139

RESULT 8  
US-10-242-535A-57254  
; Sequence 57254, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; C.I.C.: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

```

; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIORITY FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58934
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-57254

Query Match          100.0%; Score 327; DB 7; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGCCGCAGCGATGGATACCCGAGCAACAGCGGGCAAGAG 60
Db      17 ATGCCGCAGCGATGGATACCCGAGCAACAGCGGGCAAGAG 76
Qy      61 CGCTTGAAAGTGAATAACTGGAAATGCGTGGGATTTGCTGGTGTAT 120
Db      77 CGCTTGAAAGTGAATAACTGGAAATGCGTGGGATTTGCTGGTGTAT 136
Qy      1 ATGGCGCAGGGATGGATGGATGGATACCCGAGCGCACCAACACCGGGGGAAAGAG 60
Db      17 ATGGCGCAGGGATGGATGGATACCCGAGCGCACCAACACCGGGGGAAAGAG 76
Qy      61 CGCTTGAAAGTGAATAACTGGAAATGCGTGGCCCTTGCGGATATTGGTGTAT 120
Db      77 CGCTTGAAAGTGAATAACTGGAAATGCGTGGCCCTTGCGGATATTGGTGTAT 136
Qy      121 AACCTGGCCATCTGGAGCAACCACATTATGATCTTGCGATAGATGTCAGCTAACCTAG 180
Db      137 AACCTGGCCATCTGGAGCAACCACATTATGATCTTGCGATAGATGTCAGCTAACCTAG 196
Qy      181 GGCTCGCTACTTCAGAAGAGTGTACTGTGGCATGGACTCTGTAAACCATGCTTTAAC 240
Db      197 GGCTCGCTACTTCAGAAGAGTGTACTGTGGCATGGACTCTGTAAACCATGCTTTAAC 256
Qy      241 TTCCACTGCATCTCTGCTGGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 300
Db      257 TTCCACTGCATCTCTGCTGGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 316
Qy      301 TGGGATTCGAAAGATGGCTAAC 327
Db      317 TGGGATTCGAAAGATGGCTAAC 343

RESULT 9
US-10-242-535A-56068
; Sequence 56068, Application US/10242535A
; GENERAL INFORMATION:
;   Publication No. US20040013663A1
;   APPPLICANT: ChondroGene Inc.
;   INVENTION: Compositions and Methods Relating to Osteoarthritis
;   FILE REFERENCE: 4231/2005
;   CURRENT APPLICATION NUMBER: US/10/242,535A
;   CURRENT FILING DATE: 2002-09-12
;   PRIOR APPLICATION NUMBER: US 10/085,783
;   PRIOR FILING DATE: 2002-02-28
;   PRIOR APPLICATION NUMBER: US 60/305,340
;   PRIOR FILING DATE: 2001-07-13
;   PRIOR APPLICATION NUMBER: US 60/275,017
;   PRIOR FILING DATE: 2001-03-12
;   PRIOR APPLICATION NUMBER: US 60/271,955
;   PRIOR FILING DATE: 2001-02-28
;   NUMBER OF SEQ ID NOS: 58934
;   SOFTWARE: PatentIn version 3.2
SEQ ID NO: 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-56068

Query Match          100.0%; Score 327; DB 7; Length 472;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGGCGCAGCGATGGATACCCGAGCGGGACCAACAGCGGGCAAGAG 60
Db      20 ATGGCGCAGCGATGGATACCCGAGCGGGACCAACAGCGGGCAAGAG 79
Qy      61 CGCTTGAAAGTGAATAACTGGAAATGCGTGGCCCTTGCGGATATTGGTGTAT 120

```

RESULT 10  
 Sequence 56068, Application US/10085783A  
 Publication No. US2004037841A1  
 GENERAL INFORMATION:  
 APPLICANT: ChondrGene Inc.  
 ATTORNEY/AGENT: Liew, C.C.  
 TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 FILE REFERENCE: 4231/2002  
 CURRENT APPLICATION NUMBER: US/10/085,783A  
 PRIOR APPLICATION NUMBER: US 60/305,340  
 PRIOR FILING DATE: 2001-07-13  
 PRIOR APPLICATION NUMBER: US 60/275,017  
 PRIOR FILING DATE: 2001-03-12  
 PRIOR APPLICATION NUMBER: US 60/271,955  
 PRIOR FILING DATE: 2001-02-28  
 NUMBER OF SEQ ID NOS: 58994  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 56068  
 LENGTH: 472  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (437)..(437)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (455)..(455)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-085-783A-56068

Query Match 100.0%; Score 327; DB 7; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 5..6..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 80  
 LENGTH: 139  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(139)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(139)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-085-783A-56068

Query Match 100.0%; Score 327; DB 7; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 5..6..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 121  
 LENGTH: 180  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(180)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(180)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-085-783A-56068

Query Match 100.0%; Score 327; DB 7; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 5..6..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 140  
 LENGTH: 199  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(199)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(199)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-085-783A-56068

Query Match 100.0%; Score 327; DB 7; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 5..6..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 181  
 LENGTH: 240  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(240)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(240)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-085-783A-56068

Query Match 100.0%; Score 327; DB 7; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 5..6..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 200  
 LENGTH: 259  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(259)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(259)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-085-783A-56068

RESULT 11  
 Sequence 937-3  
 Publication No. US20050019813A1  
 GENERAL INFORMATION:  
 APPLICANT: Conaway, Joan A.  
 ATTORNEY/AGENT: Conway, Ronald C.  
 ATTORNEY/AGENT: Kamura, Takumi  
 ATTORNEY/AGENT: Okinoma Medical Research Foundation  
 TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
 TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase  
 FILE REFERENCE: 021044-004600US  
 CURRENT APPLICATION NUMBER: US/10/913,937  
 CURRENT FILING DATE: 2004-08-05  
 PRIORITY NUMBER: US/09/914,324  
 PRIORITY FILING DATE: 2001-08-22  
 PRIORITY APPLICATION NUMBER: US 60/121,787  
 PRIORITY FILING DATE: 1999-02-26  
 PRIORITY APPLICATION NUMBER: WO PCT/US00/04818  
 PRIORITY FILING DATE: 2000-02-25  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 508  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (7)..(333)  
 OTHER INFORMATION: Rbx1  
 US-10-913-937-3

Query Match 100.0%; Score 327; DB 8; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 5..8..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 61  
 LENGTH: 60  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (7)..(333)  
 OTHER INFORMATION: Rbx1  
 US-10-913-937-3

Query Match 100.0%; Score 327; DB 8; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 5..8..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 67  
 LENGTH: 66  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (7)..(333)  
 OTHER INFORMATION: Rbx1  
 US-10-913-937-3

Query Match 100.0%; Score 327; DB 8; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 5..8..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 181  
 LENGTH: 240  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(240)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(240)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-913-937-3

Query Match 100.0%; Score 327; DB 8; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 5..8..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 187  
 LENGTH: 246  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(246)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(246)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-913-937-3

Query Match 100.0%; Score 327; DB 8; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 5..8..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 241  
 LENGTH: 300  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(300)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(300)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-913-937-3

Query Match 100.0%; Score 327; DB 8; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 5..8..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 247  
 LENGTH: 327  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(327)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(327)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-913-937-3

Query Match 100.0%; Score 327; DB 8; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 5..8..104;  
 Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 301  
 LENGTH: 333  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(333)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(333)  
 OTHER INFORMATION: n is a, c, g, or t  
 US-10-913-937-3

RESULT 12  
 US-10-242-535A-46292  
 ; Sequence 46292, Application US/10242535A

; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY: Liew, C. C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; CURRENT FILING DATE: 2002-09-12  
; CURRENT APPLICATION NUMBER: US/10/242,515A  
; PRIORITY NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 46292  
; LENGTH: 523  
; ORGANISM: Human  
US-10-242-515A-46292

Query Match 100.0%; Score 327; DB 7; Length 523;  
Best Local Similarity 100.0%; Pred. No. 5.9e-104;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGATGGTGGATGCTGGATACCCGAGGGCAACACGGGGGGAAAGAG 60  
Db 19 ATGGCGCAGCGATGGTGGATACCCGAGGGCAACACGGGGGGAAAGAG 78

QY 61 CGCTTGAAAGTGAAGAACAGTGGAAATGGTGGATAGCTGGGCTGGGATTTGGTTAT 120  
Db 79 CGCTTGAAAGTGAAGAACAGTGGAAATGGTGGATTTGGGATTTGGTTAT 138

QY 121 AACTGTGCCATCTGGAGACCACATTATGGATCTTGGATAGATGGTGAAGTAACCG 180  
Db 139 AACTGTGCCATCTGGAGACCACATTATGGATCTTGGATAGATGGTGAAGTAACCG 198

QY 181 GCGTCGGCTACTTCAGAAGGTGTAATGTCGCATGGGAGTCTGTAAACCATGTTTAC 240  
Db 199 CGTCGGCTACTTCAGAAGGTGTAATGTCGCATGGGAGTCTGTAAACCATGTTTAC 258

QY 241 TTCCACTGCAATCTGGCTCAAACAGGAGCTGGTGTCCATTGGACAAAGAG 300  
Db 259 TTCCACTGCAATCTGGCTCAAACAGGAGCTGGTGTCCATTGGACAAAGAG 318

RESULT 14  
US-09-918-995-17191  
; Sequence 17191, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17191  
; LENGTH: 476  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(476)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-17191

Query Match 99.4%; Score 325; DB 3; Length 476;  
Best Local Similarity 100.0%; Pred. No. 2.9e-103;  
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCGCAGCGATGGATGTGGATACCCGAGGGACCAAAGCGCGCGCAAGAAGCG 62  
Db 74 GGCGCAGCGATGGATGTGGATACCCGAGGGACCAAAGCGCGCGCAAGAAGCG 133

QY 63 CTTGAAGTGAAGAACAGTGGATGGCTGGCTGGGATATGGTGTGATAA 122  
Db 134 CTTGAAGTGAAGAACAGTGGATGGCTGGCTGGGATATGGTGTGATAA 193

QY 123 CTGTCGCATCTGCAGCAACACATATGGATCTTGCATAGAAATGTCAAACAGGC 182  
SEQ ID NO 46292

Db 194 CTGTGCCATCTGAGAACACATTATGGATCTTGTATAAGTGTAAAGCTAACAGGC 253  
 Qy 183 GTCCGCTACTTCAGAAGAGTGTACTGTGATGGAGTGTAAACATGCTTTCACRT 242  
 Db 254 GTCCGCTACTTCAGAAGAGTGTACTGTGATGGAGTGTAAACATGCTTTCACRT 313  
 Qy 243 CCACTGCATCTCGTGGCTCAAACAGACAGGTGTCTGCATGGAGTGTAAACATGCTTTCACRT 302  
 Db 314 CCACTGCATCTCGTGGCTCAAACAGACAGGTGTCTGCATGGAGTGTAAACATGCTTTCACRT 373  
 Qy 303 GGAATTCCAAAGTAGTGGCACTAG 327  
 Db 374 GGAATTCCAAAGTAGTGGCACTAG 398

RESULT 15  
 US-10-198-846-11311/c  
 Sequence 11311, Application US/10198846  
 Publication No. US20030099974A1  
 GENERAL INFORMATION:  
 APPLICANT: Lillie, James  
 APPLICANT: Xu, Yongxiao  
 APPLICANT: Wang, Youhen  
 APPLICANT: Steinmann, Kathleen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TREATMENT OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198,846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 11311  
 LENGTH: 4543  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-198-846-11311

Query Match 98 4%; Score 321.8; DB 5; Length 4543;  
 Best Local Similarity 99.4%; Pred. No. 1e-10;  
 Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 APPLICANT: Steinmann, Kathleen  
 APPLICANT: Xu, Yongxiao  
 APPLICANT: Wang, Youhen  
 APPLICANT: Steinmann, Kathleen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TREATMENT OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198,846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 11311  
 LENGTH: 4543  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-198-846-11311  
 Query Match 98 4%; Score 321.8; DB 5; Length 4543;  
 Best Local Similarity 99.4%; Pred. No. 1e-10;  
 Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 APPLICANT: Steinmann, Kathleen  
 APPLICANT: Xu, Yongxiao  
 APPLICANT: Wang, Youhen  
 APPLICANT: Steinmann, Kathleen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TREATMENT OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198,846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 11311  
 LENGTH: 4543  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-198-846-11311  
 Query Match 98 4%; Score 321.8; DB 5; Length 4543;  
 Best Local Similarity 99.4%; Pred. No. 1e-10;  
 Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 APPLICANT: Steinmann, Kathleen  
 APPLICANT: Xu, Yongxiao  
 APPLICANT: Wang, Youhen  
 APPLICANT: Steinmann, Kathleen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TREATMENT OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198,846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 11311  
 LENGTH: 4543  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-198-846-11311  
 Query Match 98 4%; Score 321.8; DB 5; Length 4543;  
 Best Local Similarity 99.4%; Pred. No. 1e-10;  
 Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

This Page Blank (uspic)

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

CM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 15:48:59 ; Search time 291.318 Seconds

(without alignments)  
 2589.902 Million cell updates/sec

Title: US-09-541-462B-1  
 Perfect score: 327

Sequence: 1 argccggcagcgatggatgt.....tccaaaaatggcactag 327

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters:

15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$

Maximum Match 100\$

Listing first 45 summaries

Database : Published Applications NA\_New:\*

```

 1: /cgn2_6/prodata/2/pubnpna/US08_NEW_PUB.seq;*
 2: /cgn2_6/prodata/2/pubnpna/US05_NEW_PUB.seq;*
 3: /cgn2_6/prodata/2/pubnpna/US07_NEW_PUB.seq;*
 4: /cgn2_6/prodata/2/pubnpna/PCT_NEW_PUB.seq;*
 5: /cgn2_6/prodata/2/pubnpna/US05_NEW_PUB.seq;*
 6: /cgn2_6/prodata/2/pubnpna/US09_NEW_PUB.seq;*
 7: /cgn2_6/prodata/2/pubnpna/US10_NEW_PUB.seq;*
 8: /cgn2_6/prodata/2/pubnpna/US10_NEW_PUB.seq;*
 9: /cgn2_6/prodata/2/pubnpna/US11_NEW_PUB.seq;*
10: /cgn2_6/prodata/2/pubnpna/US11_NEW_PUB.seq2;*
11: /cgn2_6/prodata/2/pubnpna/US11_NEW_PUB.seq3;*
12: /cgn2_6/prodata/2/pubnpna/US11_NEW_PUB.seq4;*
13: /cgn2_6/prodata/2/pubnpna/US00_NEW_PUB.seq;*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	177.2	54.2	660	9 US-11-096-568A-11809	Sequence 11809, A
2	177.2	54.2	693	9 US-11-096-568A-26820	Sequence 26820, A
3	172.4	52.7	348	9 US-11-096-568A-28569	Sequence 28569, A
4	169.8	51.9	432	9 US-11-096-568A-14405	Sequence 14405, A
5	130	39.8	366	7 US-10-932-182A-2279	Sequence 2279, Ap
6	130	39.8	366	7 US-10-932-182A-2279	Sequence 2279, Ap
7	123.6	37.8	366	7 US-10-932-182A-78459	Sequence 78459, A
8	123.6	37.8	366	7 US-10-932-182A-78459	Sequence 78459, A
9	76	23.2	342	8 US-10-821-234-554	Sequence 554, App
c 10	74	22.6	153	7 US-10-932-182A-81177	Sequence 81177, A
c 11	74	22.6	153	7 US-10-932-182A-81177	Sequence 81177, A
12	68.2	20.9	546	12 US-11-128-061-5740	Sequence 5740, Ap
13	68.2	20.9	546	12 US-11-128-049-5740	Sequence 5740, Ap
14	68.2	20.9	579	12 US-11-128-061-2098	Sequence 2098, Ap
15	68.2	20.9	579	12 US-11-128-049-2098	Sequence 2098, Ap
c 16	65.4	20.0	207	7 US-10-932-182A-6146	Sequence 6146, Ap
c 17	65.4	20.0	207	7 US-10-932-182A-6146	Sequence 6146, Ap
18	42.8	13.1	450	9 US-11-057-484A-14	Sequence 14, App
19	39.6	12.1	3404	12 US-11-045-468A-18	Sequence 18, App
20	34.2	10.5	201	8 US-10-995-561-20992	Sequence 20992, A

RESULT 1  
 US-11-096-568A-11809  
 ; Sequence 11809, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; TITLE OF INVENTION: Theory  
 ; FILE REFERENCE: 2750-159PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096, 568A  
 ; CURRENT FILING DATE: 2006-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO 11809  
 ; LENGTH: 660  
 ; TYPE: DNA  
 ; ORGANISM: triticum aestivum  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1) (660)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 13657464  
 US-11-096-568A-11809

Query Match Score 54.2%; Best Local Similarity 58.5%; Pred. No. 3.2+46; Matches 212; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 58 AAGGCCCTTGAAAGTGAATGGGATAGCCCTGGGATATTGGTT  
 Db 193 AAGGCCCTTGAAAGTGAATGGGATATTGGGATGGACATCTGGT  
 Qy 118 GATAACTGTGCCATCTGCCAACATATTGGATCTTCATGAAAGTCAAC 177  
 Db 253 GACAATGCCCATCTGCCAACATCATGGATTATGCATGAGTCGCCAAC 312  
 Qy 178 CAGGGTCGGCTTAATGGTCAAAGACTGTAATGTGCCATGGCTTT 237  
 Db 313 CAGGCCAGGCCAACAGCAGGATGTCACCGTCCATGGGTGCTGTAAATCAGCTTC 372  
 Qy 238 CACTCCACTGCACTCTCGCTGGCTCAAACAGCACAGGTGTCATGGACAGCA 297  
 Db 373 CACTCCACTGCACTGAGTGGCTAAAGTCGCAACTAGAACAGC 432  
 Qy 298 GAGTGGGAATTCCAAAAGTATGGGCACTAG 327

RESULT 2  
 US-11-096-568A-26820  
 ; Sequence 28820, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; TITLE OF INVENTION: Therby  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096, 568A  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO: 26820  
 ; LENGTH: 693  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays subsp. mays  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(693)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 13622871  
 US-11-096-568A-26820

Query Match 52.7%; Score 172.4; DB 9; Length 348;  
 Best Local Similarity 77.4%; Pred. No. 0; Mismatches 61; Indels 0; Gaps 0;

Qy 57 GAAGCGCTTTGAGTGGAAAAGTGGAATGCACTGAGCTTCGGGATATGCGGT 116  
 Db 78 GAAACGATTGAAATTAAGAAGTGGATCTGGATGGATCTGGCTGTGT 137

Qy 117 TGATAACTGTGCCATTGCGGAAACCACATTAGATCTTGATAGATGGTCAAGCTAA 176  
 Db 138 TGATAACTGCGCAATTCTAGGATCATCAAGTCACTGTGATGGTCAAGCTAA 197

Qy 177 CCAGCGCTCGGTTACTCAGAACAGTGTACTGCGCTAACCTGCTT 236  
 Db 198 TCAAGCTTAGTGCCATTAGTGAAATGCACTGTGCTGGGCTTCAACCGCTT 257

Qy 237 TCACTTCCACTGCATCTCGCTGGCTCAAAACCGAAGGGTGTCCATTGGACACAG 296  
 Db 258 TCACTTCCACTGTATCACGAGATGGCTCAAACCTGTCAAGTGTCCACTAGATGTCTG 317

Qy 297 AGAGTGGGAATTCCAAAAGTATGGCAGTAA 326  
 Db 318 CGACTGGGAATTCCAGAAATATGGTCACTA 347

RESULT 4  
 US-11-096-568A-14405  
 ; Sequence 14405, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Therby  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096, 568A  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO: 14405  
 ; LENGTH: 432  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays subsp. mays  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(432)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 4776740  
 US-11-096-568A-14405

Query Match 51.9%; Score 169.8; DB 9; Length 432;  
 Best Local Similarity 77.0%; Pred. No. 6.2e-44; Mismatches 0; Indels 0; Gaps 0;

Qy 58 AAGGCCTTGAAGTGGAAAAGTGGGATGAGCTGGCTGGGATATTGGGTT 117  
 Db 171 AAGCCCTTCGAGATAAGAGTGGAAACGGCTGGGCTGGCTGGCATGTGTTG 230

Qy 118 GATAACTGSGCCATCTGAGGAACCAATTATGGATCTTGCATAAGTCAAGCTAAC 177  
 Db 231 GACAATGCCCATCTGCCAAACACATGAGACCTTGCATGCCAGGGGAAAC 290

Qy 178 CAGGCCCTGCACTCTCCTCGCTGGCTCAAAACACGACAGTGTGTCATGGCACT 237  
 Db 291 CAGGGAGGCCACAGGGAGTCACGGTGGGAATTGGCAACCATGCACTTC 350

Qy 238 CACTTCCACTGCACTCTCCTCGCTGGCTCAAAACACGACAGTGTGTCATGGCACT 297  
 Db 351 CACTTCACTCTATGGCTGGTAAGAACCCGTCAAAGTGTGCCCTTGACACAGT 410

Qy 298 GAGTGGGAATTCCAAAAGTATGGGACTAG 327  
 Db 411 GAGTGGGAATTCCAGAGATGGTCACTAG 440

RESULT 3  
 US-11-096-568A-28569  
 ; Sequence 28569, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; TITLE OF INVENTION: Therby  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096, 568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO: 28569  
 ; LENGTH: 348  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(348)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 3017472  
 US-11-096-568A-28569

Qy 58 CACTTCACTGCACTCTCCTGGCTGAAACATATGGATCTGGTCAAGCTAA 117  
 Db 161 AAGGAAATTGCAAGTAAAGGTGGCTGGGATATCGGT 220

Qy 118 GATAACTGCGCATCTGCAAAACACATATGGATCTGGTCAAGCTAA 177  
 Db 221 GACAATGGCGCATCTGCAAAACACATATGGATCTGGTCAAGCTAA 280

Qy 178 CAGGGCTCCGCTACTTCAGAAGAGTGTACTGCTGGATGGGAGTGTCAACATGGCTT 237  
 Db 281 CAGGCCAGCGCTAACGGTGGAAATGCACTGTGGCTGGGGTTGCAATTCACGCCCTC 340

Qy 238 GAGTGGGAATTCCAAAAGTATGGGACTAG 326  
 Db 401 GAGTGGGAATTCCAGAGATGGTCACTA 429

US-10-932-182A-2279  
*i* Sequence 2279, Application US/10932182A  
*i* Publication No. US200604625A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: NAKAO, YOSHIHIRO  
*i* APPLICANT: NAKAMURA, NORIHIRO SA  
*i* APPLICANT: KODAMA, YUKIKO  
*i* APPLICANT: FUJIMURA, TOMOKO  
*i* APPLICANT: ASHIKARI, TOSHIHIKO  
*i* TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
*i* FILE REFERENCE: 030685-043  
*i* CURRENT APPLICATION NUMBER: US/10/932,182A  
*i* CURRENT FILING DATE: 2004-09-02  
*i* NUMBER OF SEQ ID NOS: 197023  
*i* SOFTWARE: PatentIn version 3.3  
*i* SEQ ID NO: 2279  
*i* LENGTH: 366  
*i* TYPE: DNA  
*i* ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-2279

Query Match 39.8%; Score 130; DB 7; Length 366;  
Best Local Similarity 68.0%; Pred. No. 2.6e-31;  
Matches 181; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Db 94 AAAAGAGATTGGAGTTAAATAATGACAGGGCCTGGGTCTGGGATATAGCC 153  
Qy 115 GTTGATAACTTGCCTCATGGGACCATTAATGGATCTGGCTAGAAATGTCAGCT 174  
Db 154 GTTGACAAGTGGCAATTGGGATGGGAACTGGGATGGGATGGGATGGG 213  
Qy 175 AACAGGGCTCGCTACTTCGAAGAGTGTGCTGGGATGGGATGGGATGGG 234  
Db 214 TTCCACTTGCACATGCAATAAGGATGTGGAGCATGGGTGTAATAGCT 273  
Qy 235 TTTCACTTCCACTGCATCTCGCGGCTCAAACAGACAGGGTGTGTCATTGGACAC 294  
Db 274 AACCAGCGTGCCTCATTCGAAGAGTGTGACTGTGCACTGGGACTGG 320  
Qy 295 AGAGACTGGGATTCAAAAAGTATGG 320  
Db 334 CAACCTTGGCAATTGGCAAGGTGG 359

RESULT 6  
US-10-932-182A-2279  
*i* Sequence 2279, Application US/10932182A  
*i* Publication No. US200604625A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: NAKAO, YOSHIHIRO  
*i* APPLICANT: NAKAMURA, NORIHIRO SA  
*i* APPLICANT: KODAMA, YUKIKO  
*i* APPLICANT: FUJIMURA, TOMOKO  
*i* APPLICANT: ASHIKARI, TOSHIHIKO  
*i* TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
*i* FILE REFERENCE: 030685-043  
*i* CURRENT APPLICATION NUMBER: US/10/932,182A  
*i* CURRENT FILING DATE: 2004-09-02  
*i* NUMBER OF SEQ ID NOS: 197023  
*i* SOFTWARE: PatentIn version 3.3  
*i* SEQ ID NO: 2279  
*i* LENGTH: 366  
*i* TYPE: DNA  
*i* ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-2279

Query Match 39.8%; Score 130; DB 7; Length 366;  
Best Local Similarity 68.0%; Pred. No. 2.6e-31;  
Matches 181; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Db 94 AAAAGAGATTGGAGTTAAATAATGACAGGGCCTGGGTCTGGGATATAGCC 153  
Qy 115 GTTGATAACTTGCCTCATGGGACCATTAATGGATCTGGCTAGAAATGTCAGCT 174  
Db 154 GTTGACAAGTGGCAATTGGGATGGGAACTGGGATGGGATGGGATGGG 213  
Qy 175 AACAGGGCTCGCTACTTCGAAGAGTGTGCTGGGATGGGATGGGATGGG 234  
Db 214 TTCCACTTGCACATGCAATAAGGATGTGGAGCATGGGTGTAATAGCT 273  
Qy 235 TTTCACTTCCACTGCATCTCGCGGCTCAAACAGACAGGGTGTGTCATTGGACAC 294  
Db 274 AACCAGCGTGCCTCATTCGAAGAGTGTGACTGTGCACTGGGACTGG 320  
Qy 295 AGAGACTGGGATTCAAAAAGTATGG 320  
Db 334 CAACCTTGGCAATTGGCAAGGTGG 359

RESULT 7  
US-10-932-182A-78459  
*i* Sequence 78459, Application US/10932182A  
*i* Publication No. US200604625A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: NAKAO, YOSHIHIRO  
*i* APPLICANT: FUJIMURA, NORIHIRO  
*i* APPLICANT: KODAMA, YUKIKO  
*i* APPLICANT: ASHIKARI, TOSHIHIKO  
*i* TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
*i* FILE REFERENCE: 030685-043  
*i* CURRENT APPLICATION NUMBER: US/10/932,182A  
*i* CURRENT FILING DATE: 2004-09-02  
*i* NUMBER OF SEQ ID NOS: 197023  
*i* SOFTWARE: PatentIn version 3.3  
*i* SEQ ID NO: 78459  
*i* LENGTH: 366  
*i* TYPE: DNA  
*i* ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-78459

Query Match 37.8%; Score 123.6; DB 7; Length 366;  
Best Local Similarity 66.5%; Pred. No. 2.8e-29;  
Matches 177; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Db 94 AAAAGAGATTGGAAATGGGATGGCTGGGCTCTGGGATATTGG 114  
Qy 115 GTTGATAACTTGCCTCATGGGACCATTAATGGATCTGGCTAGAAATGTCAGCT 153  
Db 154 GTTGACAAGTGGCAATTGGGATGGGAACTGGGATGGGATGGG 213  
Qy 175 AACAGGGCTCGCTACTTCGAAGAGTGTGCTGGGATGGGATGGGATGGG 234  
Db 214 TTCCACTTGCACATGCAATAAGGATGTGGAGCATGGGTGTAATAGCT 273  
Qy 235 TTTCACTTCCACTGCATCTCGCGGCTCAAACAGACAGGGTGTGTCATTGGACAC 294  
Db 274 AACCAGCGTGCCTCATTCGAAGAGTGTGACTGTGCACTGGGACTGG 320  
Qy 295 AGAGACTGGGATTCAAAAAGTATGG 320  
Db 334 CAACCTTGGCAATTGGCAAGGTGG 359

RESULT 8  
US-10-932-182A-78459  
*i* Sequence 78459, Application US/10932182A  
*i* Publication No. US200604625A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIKO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TONOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 78459  
; LENGTH: 366  
; TYPE: DNA  
; ORGANISM: *Saccharomyces pastorianus*  
; US-10-932-182A-78459

Query Match 37.8%; Score 123.6; DB 7; Length 366;  
Best Local Similarity 66.5%; Pred. No. 2.8e-29; Indels 0; Gaps 0;  
Matches 177; Conservative 0; Mismatches 89;

QY 55 AAGAGCGCTTGAAGTGAANAACTGGATTGCAACTAGGCCCTCTGGCTGGATGATTTGTG 114  
DB 94 AAGAGAGATTGAAATTAGAAATGGACCAGTGGGTTGGTCATGGGATATAGCT 153  
QY 115 GTTGATAACTGTGCCATTGAGAACACATTATGGATCTTCATAGAAATTCAAAGCT 174  
DB 154 GTTGACAACGTGTGTTATTTGAGAACATATGGACCATGGTGTGTTGGCAGCA 213  
QY 175 AACCAAGCCCTCGCTACTTCAGAGAGTGTACTGCGATGGGGAGTGTGTAACCAGCT 234  
DB 214 AAGGCCATAGGGAGACATGATAATGAAATGTGAGCTGGGTGTGTAATCACGCT 273  
QY 235 TTTCACTTCACTGATGATCTCGTGGTCAACCATGGTGTGTCATGGACAC 294  
DB 274 TTCCATTGCACTGTATTAATGGATCAAGAACGACATGGCCATTAGATAAAC 333  
QY 295 AGAGATGGGAATTCCAAGAACTATGG 320  
DB 334 CAACCTTGGAGTTAGCAAGATGGG 359

RESULT 9  
US-10-821-234-554  
; Sequence 554, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; PRIOR FILING DATE: 2004-04-07  
; CURRENT FILING DATE: 2004-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_SEQ\_genes Version 1.0  
; SEQ ID NO: 554  
; LENGTH: 342  
; TYPE: DNA  
; ORGANISM: *Homo sapiens*  
; US-10-821-234-554

Query Match 23.2%; Score 76; DB 8; Length 342;  
Best Local Similarity 56.9%; Pred. No. 3.5e-14;  
Matches 164; Conservative 0; Mismatches 115; Indels 9; Gaps 1;

QY 26 CCCCAGGGGACCAACAGCGCCGGCAGAACGCCCTTGAACTGAAAGCTGCAATG 85  
DB 50 CGGGAGCTCAGGTCCTCAAGTCGGAGGCAGTCAGTGTCTCCCTCAAGAAGTCGAACG 109  
QY 86 CAGTACCCCTGGGCTGGGATATGTGTCATCTGAGAACCCACA 145

RESULT 10  
US-10-932-182A-81177/C  
; Sequence 81177, Application US/10932182A  
; Publication No. US2006004253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIKO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TONOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 81177  
; LENGTH: 153  
; TYPE: DNA  
; ORGANISM: *Saccharomyces pastorianus*  
; US-10-932-182A-81177

Query Match 22.6%; Score 74; DB 7; Length 153;  
Best Local Similarity 75.4%; Pred. No. 1.2e-13;  
Matches 92; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 55 AAGAGCGCTTGAAGTGAANAACTGGATGCAACTAGGCCCTCTGGCTGGATGATTTGTG 114  
DB 128 AAGAGAGATTGAAATTAGAAATGGACCAGTGGGTTGGTCATGGGATATAGCT 69  
QY 115 GTTGATAACTGTGCCATTGAGAACACATTATGGACCATGGTGTGTCATAGAATGTCAAGT 174  
DB 68 GTTGACAACGTGTGTTGGCAGCTGGGTGTGTAATCACGCT 9  
QY 175 AA 176  
DB 8 AA 7

RESULT 11  
US-10-932-182A-81177/C  
; Sequence 81177, Application US/10932182A  
; Publication No. US2006004253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIKO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TONOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 81177  
; LENGTH: 153



US-11-128-061-2098

APPLICANT: Brown, Eugene L.  
; APPLICANT: Miller, Christopher P.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION  
; FILE REFERENCE: 01937-057701  
; CURRENT APPLICATION NUMBER: US/11/128,061  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US 60/570,425  
; PRIOR FILING DATE: 2004-05-11  
; NUMBER OF SEQ ID NOS: 7285  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO: 2098  
; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: Cricetulus griseus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (122)-(154)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (547)-(568)  
; OTHER INFORMATION: n is a, c, g, or t

Query	Match	Score	Length
Best Local Matches	Similarity	Pred. No.	
Qy	Qy	1.3e-11;	1
Db	Db	0;	Mismatches
Qy	Qy	143;	Conservative
Db	Db	125;	Indels
Qy	Qy	9;	Gaps
Db	Db	108;	
Qy	Qy	108;	
Db	Db	124;	
Qy	Qy	168;	
Db	Db	184;	
Qy	Qy	228;	
Db	Db	235;	
Qy	Qy	288;	
Db	Db	295;	
Qy	Qy	325;	
Db	Db	332;	

RESULT 15  
US-11-128-049-2098  
Sequence : 2098, Application US/11128049  
; Publication No. US20060010513A1  
GENERAL INFORMATION:  
; APPLICANT: Melville, Mark W.  
; APPLICANT: Charlebois, Timothy S.  
; APPLICANT: Mounts, William M.  
; APPLICANT: Hann, Louane E.  
; APPLICANT: Sinacore, Martin S.  
; APPLICANT: Leonard, Mark W.  
; APPLICANT: Brown, Eugene L.  
; APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
; TITLE OF INVENTION: MAKING AND USING SAME  
; FILE REFERENCE: 01997 02 07700  
; CURRENT APPLICATION NUMBER: US/11/128,049  
; CURRENT FILING DATE: 2005-05-11  
; PRIORITY APPLICATION NUMBER: US 60/570,425  
; PRIORITY FILING DATE: 2004-05-11  
; NUMBER OF SEQ ID NOS: 7285  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 2098

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 14:34:46 ; Search time 98.7354 Seconds  
(without alignments)  
5887.073 Million cell updates/sec

Title: US-09-541-462B-1  
Perfect score: 327  
Sequence: 1.atggccgagatggatgt.....tccaaaaatggcactag 327

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 88780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$  
Maximum Match 100\$  
Listing first 45 summaries

Database : Issued\_Patent\_NA:  
1: /cggn2\_6/prodata/1/ina/1-COMB.seq:  
2: /cggn2\_6/prodata/1/ina/5-COMB.seq:  
3: /cggn2\_6/prodata/1/ina/6-COMB.seq:  
4: /cggn2\_6/prodata/1/ina/6B-COMB.seq:  
5: /cggn2\_6/prodata/1/ina/H-COMB.seq:  
6: /cggn2\_6/prodata/1/ina/PCTUS-COMB.seq:  
7: /cggn2\_6/prodata/1/ina/PP-COMB.seq:  
8: /cggn2\_6/prodata/1/ina/RE-COMB.seq:  
9: /cggn2\_6/prodata/1/ina/backfile1.seq:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

RESULT 1  
US-09-513-999C-3894  
Sequence 3894, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J. B.  
; ATTORNEY: Ducleir, A.  
; APPLICANT: Giordano, J. Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIORITY APPLICATION NUMBER: US 60/122,487  
; PRIORITY FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SRQ ID NO: 3894  
; LENGTH: 482  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 29..352  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 401  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 404  
; OTHER INFORMATION: m=a or c

Query Match Length DB ID Description

1 327 100.0 482 3 US-09-513-999C-3894 Sequence 3894, AP  
2 327 100.0 507 3 US-09-541-016-3940 Sequence 4940, AP  
3 327 100.0 508 3 US-09-914-324A-3 Sequence 3, Appli  
4 290.2 88.7 504 3 US-09-914-324A-5 Sequence 5, Appli  
5 253.6 77.6 3208 3 US-09-180-016-27 Sequence 27, Appli  
6 253.6 77.6 3208 3 US-10-214-811-27 Sequence 27, Appli  
7 253.6 77.6 3208 3 US-10-766-074-27 Sequence 27, Appli  
8 170 52.0 402 3 US-09-513-999C-10371 Sequence 10371, A  
9 170 52.0 463 3 US-09-621-976-15180 Sequence 15180, A  
10 153.2 46.9 411 3 US-09-640-211A-1731 Sequence 1731, A  
C 11 138.2 42.3 490 3 US-09-270-0767-28812 Sequence 26812, A  
C 12 138.2 42.3 1101 3 US-09-270-0767-11265 Sequence 11265, A  
13 123.6 37.8 480 3 US-09-914-324A-4 Sequence 4, Appli  
14 114.4 35.0 357 3 US-09-248-074-27 Sequence 5495, AP  
15 92.6 28.3 25274 3 US-09-949-016-16682 Sequence 16582, A  
16 90 27.5 301 3 US-09-313-294A-492 Sequence 492, App  
17 74 22.6 342 3 US-09-826-312A-7 Sequence 7, Appli  
18 74 22.6 342 3 US-09-542-497A-7 Sequence 7, Appli  
19 74 22.6 342 3 US-10-108-767-7 Sequence 7, Appli  
20 46.4 14.2 439 3 US-09-799-051-296 Sequence 296, App  
21 36 11.0 601 3 US-09-949-016-174803 Sequence 174803, App  
22 33.6 10.3 87734 3 US-09-949-016-174803 Sequence 174803, App  
C 23 33.4 10.2 170 3 US-09-270-0767-26253 Sequence 26253, A  
C 24 33.4 10.2 585 3 US-09-270-0767-10788 Sequence 10788, A

Query Match Length DB ID Description

Qy 1 ATGGGGCAAGGCGATGGATGTGGATACCCGAGGCCAACAGGGCGGGCAAGAG 60  
29 ATGGGGCAAGGCGATGGATACCCGAGGCCAACAGGGCGGGCAAGAG 88  
Db 61 CGTTTGAAGTGAAGAAAGTGGAAATCGTACGCCCCCTGGCCCTGGATATTGGTGTGAT 120  
89 CGTTTGAAGTGAAGAAAGTGGAAATCGTACGCCCCCTGGCCCTGGATATTGGTGTGAT 148  
Qy

db	149	AACTGTGCCATCTGGAGAACACATAATGGATCTTGCATAAGATGCAAGTCACCG	208
yy	181	GCTCCGGTACTCTAGAAGAGTGACTCTGCAATGGGAGATCTGTAACCAGTTTCAC	240
db	209	GCTCCGGTACTCTAGAAGAGTGACTCTGCAATGGGAGATCTGTAACCAGTTTCAC	268
yy	241	TTCGACTGCCATCTCTCGTGGCTAAACACGACAGGTGTCATGGACACAGAGAG	300
db	269	TTCGACTGCCATCTCTCGTGGCTAAACACGACAGGTGTCATGGACACAGAGAG	328
yy	301	TGGGAATTCAAAAGTATGGCACTAG	327
db	329	TGGGAATTCAAAAGTATGGCACTAG	355

RESULT 2  
US-09-949-016-4940  
Sequence 4940, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 4940  
LENGTH: 507  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-4940

```

; Software: Falcultin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1
US-09-914-324A-3

Query Match      100.0%; Score 327; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 3. 4e-103; Mismatches 0; Indels 0
Matches 327; Conservative 0; Mismatches 0; Indels 0

Qy   1 ATGGCGGAGCGATGGATGTGGATAACCCGAGGGACCAACAGCGCGCCG
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   7 ATGGCGGAGCGATGGATGTGGATAACCCGAGGGACCAACAGCGCGCCG
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   61 CGCTTGTGAGTAAAAACTGGATGGCTCTGGCTGGATATTC
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   67 CGCTTGTGAGTAAAAACTGGATGGCTCTGGCTGGATATTC
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   121 ACTGTGGCATCTGCAGGAACACATTATGGATCTTGCATGAATCTCAAC
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Query	Match	Score	DB 3:	Length
	Best Local Similarity	100.0%	Score 327;	507;
	Matches	100.0%	Pred. No.	3.3e-103;
	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0
Qy	1 ATGCCGGCAGCGATGGATGTGGATAACCCGAGGCCACCAACGCCGGCCGGCAAGAGAG 60			
Db	7 ATGCCGGCAGCGAGGGATCTGGATAACCCGAGGCCACCAACAGGGCGGGCAAGAGAG 66			
Qy	61 CGCTTGAAGTGAAGAAAGTGGAAATGCAAGTGCAGTCAGCCCTCTGGCCCTGGATATTGTTGTAT 120			
Db	67 CGCTTGAAGTGAAGAAAGTGGAAATGCAAGTGCAGTCAGCCCTCTGGCCCTGGATATTGTTGTAT 126			
Qy	121 AACTGTGCCATCTCAGGAACCAATTATGGATCTTGATGAAATGTCAGCTAACAG 180			
Db	127 AACTGTGCCATCTCAGGAACCAATTATGGATCTTGATGAAATGTCAGCTAACAG 186			
Qy	181 GCGTCGGTACTCTAGAAAGTGTACTGTGCGATGGGAGTCCTTAACCATGCTTTTCAC 240			
Db	187 GCGTCGGTACTCTAGAAAGTGTACTGTGCGATGGGAGTCCTTAACCATGCTTTTCAC 246			
Qy	241 TTCACTGTGATCTCGCTGGCTCAAACAGCAGGTGTCCATTGGACAAAGAGAG 300			
Db	247 TTCACTGTGATCTCGCTGGCTCAAACAGCAGGTGTCCATTGGACAAAGAGAG 306			
Qy	301 TGGGAATTCCAAAAGTATGGGCACTAG 327			
Db	307 TGGGAATTCCAAAAGTATGGGCACTAG 333			

PRIOR FILING DATE: 2000-02-25  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 5  
 LENGTH: 504  
 TYPE: DNA  
 ORGANISM: Mus sp.  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1..8) ..(344)  
 OTHER INFORMATION: Rbx1

US-00-914-324A-5

Query Match Score 88.7%; DB 3; Length 504;  
 Best Local Similarity 93.0%; Pred. No. 2e-90;  
 Matches 304; Conservative 0; Mismatches 23;  
 Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGTGGATGGGATAACCCGGGGCAGAACAGGGGGAAAGAG 60  
 Db 18 ATGGCGGGGGATGGATGGATGGATACCCCGAGGGCACAAACGGGGCAAGAG 77

Qy 61 CGCTTGAAGTAAAAAGTGGAAATGGCACTAGGCCCTCTGGCTGGATATTGGTGTAT 120  
 Db 78 CGTTTGAACTTAAAGTGGATGGCAATGGGCTCTGGCTGGACATGGTGTAT 137

Qy 121 AACTGTGCATCTGCGGAAACCACATTAGATCTTCATAGAATGTCAAGTAACAG 180  
 Db 138 AACTGTGCATCTGCGGAAACCACATTAGATCTTCATAGAATGTCAAGGCACAG 197

Qy 181 GCCTCCGTACTTCAAGAAGTGTACTGTGGATGGAGCTGTAA CCTGGTTTAC 240  
 Db 198 GCCTCAGTCACTTCCGAGAGTGTACGGTTGCAACCAGTGTTCAT 257

Qy 241 TTCCACTGCACTCTCGCTGTGTCAAACAGCACAGGTGTGTCATGGACAGAG 300  
 Db 258 TTCCACTGCACTCTCGCTGTGTCAAACAGAGCAGGTGTGTCATGGACAGAG 317

Qy 301 TGGGAATCCAAAAGTGGCACTAG 327  
 Db 318 TGGGAGTCCAGAGTATGGCATTAG 344

RESULT 5  
 US-00-780-016-27  
 ; Sequence 27, Application US/09780016  
 ; Patent No. 6509456  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donoho, Gregory  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Abuin, Alejandro  
 ; APPLICANT: Zambrowicz, Brian  
 ; APPLICANT: Sands, Arthur T.  
 ; TITLE OF INVENTION: No. 650456el Human Proteases and  
 ; Polynucleotides Encoding the Same  
 ; FILE REFERENCE: LEX-0132-US-A  
 ; CURRENT APPLICATION NUMBER: US/10/214, 811  
 ; CURRENT FILING DATE: 2002-08-07  
 ; PRIOR APPLICATION NUMBER: US/09/780, 016  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIORITY NUMBER: US 60/181, 294  
 ; PRIORITY FILING DATE: 2000-02-11  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SEQ ID NO 27  
 ; LENGTH: 3208  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-214-811-27

Query Match Score 77.6%; DB 3; Length 3208;  
 Best Local Similarity 98.5%; Pred. No. 2.6e-77;  
 Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 68 AAGTGAAGTGGAAATGGCACTTGGCTGGATATTGGTGTATACTGTG 127  
 Db 2765 AAAAAGAAAATGGATGGTGTGCACTTGGCTGGATATTGGTGTATACTGTG 2824

Qy 128 CCATCTGCGGAAACCACATTAGATCTTGATAGAATGTCAACCTAACGGGCTCCG 187  
 Db 2825 CCATCTGCGGAAACCACATTAGATCTTGATAGAATGTCAACCTAACGGGCTCCG 2884

Qy 188 CTACTTCAAGAGTGTACTGTGGATCTGTCAACCATGGTTTCACTTCACAT 247  
 Db 2885 CTACTTCAAGAGTGTACTGTGGATCTGTCAACCATGGTTTCACTTCACAT 2944

Qy 248 GCATCTCTGGCTGGTCAAAACACGCAAGGTGTICATGGACAAACAGAGTGGGAAT 307  
 Db 2945 GCATCTCTGGCTGGTCAAAACACGCAAGGTGTICATGGACAAACAGAGTGGGAAT 3004

Qy 308 TCCAAAAGTGGCACTAG 327  
 Db 3005 TCCAAAAGTGGCACTAG 3024

Qy 3005 TCCAAAAGTGGCACTAG 3024

```

RESULT 7
US-10-766-074-27
; Sequence 27, Application US/10766074
; Patent No. 681563
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn.
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Human Proteases and Polynucleotides Encoding the Same
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US 10/766,074
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/10/214,811
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-766-074-27

Query Match 77 6%; Score 253 6; DB 3; Length 3208;
Best Local Similarity 98.5%; Fred. No. 2.6e-77; Indels 0; Gaps 0;
Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 68 AAGTAAAGTGGATGCACTAGCCTCTGGCTGGATATTGGTTGATAACTGTG 127
Db 2765 AAAAAGAAATGGATGCACTAGCCTCTGGCTGGATATTGGTTGATAACTGTG 2824

Qy 128 CCATCTGCAGAACACATTGGATCATGGCTTCATGGATTAACGGCTCCG 187
Db 2825 CCATCTGCAGAACACATTGGATCTTGGATCATGGATTAACGGCTCCG 2884

Qy 188 CTACTTCAGAAAGAGTGACTGTGGAGTCGTGTAACATGCTTTCACTTCCACT 247
Db 2885 CTACTTCAGAAAGAGTGACTGTGGAGTCGTGTAACATGCTTTCACTTCCACT 2944

Qy 248 GCATCTCTGGTGGCTAACACAGCAGGTGTGTCATTGCAACAGAGTGGGAAT 307
Db 2945 GCATCTCTGGTGGCTAACACAGCAGGTGTGTCATTGCAACAGAGTGGGAAT 3004

Qy 308 TCCAAAAGTAGTGGGCACTAG 327
Db 3005 TCCAAAAGTAGTGGGCACTAG 3024

RESULT 8
US-09-513-999C-10371
; Sequence 10371, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Duclerc, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE US-2/REG: 59.US2
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; SOFTWARE: Patent .pm
; NUMBER OF SEQ ID NOS: 36681
; NUMBER OF SEQ ID NOS: 36681
; LENGTH: 402
; SEQ ID NO: 10371
; TYPE: DNA
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 20
; OTHER INFORMATION: k=g or t
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 38
; OTHER INFORMATION: s=g or c
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 79
; OTHER INFORMATION: n=a, g, c or t
; US-09-513-999C-10371

Query Match 52.0%; Score 170; DB 3; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-48; Mismatches 0; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGATGTCAGTACCAAGGGTGGTACTTCAGAAGGTGACTGTGCAATGGG 217
Db 106 GCATAGATGTCAGTACCAAGGGTGGTACTTCAGAAGGTGACTGTGCAATGGG 165

Qy 218 GAGTCGTAAACCATGCTTTCACTTCACGCACTGCACTGCTGGCTCAAACACGAG 277
Db 166 GAGTCGTAAACCATGCTTTCACTTCACGCACTGCACTGCTGGCTCAAACACGAG 225

Qy 278 TGTTGTCATTGGCAACAGAGTGGGAATTCCAAAATATGGGCACTAG 327
Db 226 TGTTGTCATTGGCAACAGAGTGGGAATTCCAAAATATGGGCACTAG 275

RESULT 9
US-09-621-976-15180
; Sequence 15180, Application US/09621976
; Patent No. 6633063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET_054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent .pm
; SEQ ID NO: 15180
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 74
; OTHER INFORMATION: n=a, g, c or t
; US-09-621-976-15180

Query Match 52.0%; Score 170; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Mismatches 0; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGATGTCAGTACCAAGGGTGGTACTTCAGAAGGTGACTGTGCAATGGG 217
Db 101 GCATAGATGTCAGTACCAAGGGTGGTACTTCAGAAGGTGACTGTGCAATGGG 160

Qy 218 GAGTCGTAAACCATGCTTTCACTTCACGCACTGCACTGCTGGCTCAAACACGAG 277
Db 161 GAGTCGTAAACCATGCTTTCACTTCACGCACTGCACTGCTGGCTCAAACACGAG 220

```

Qy 278 TGTGTCATTGGACAAAGAGAGTGGGAATTCCAAAAGTATGGCACACTAG 327  
 Db 221 TGTGTCATTGGACAAAGAGAGTGGGAATTCCAAAAGTATGGCACACTAG 270

**RESULT 10**  
 US-09-640-211A-1731  
 Sequence 1731 Application US/09640211A  
 ; Patent No. 6832446

; GENERAL INFORMATION:  
 ; APPLICANT: Wood, Marion  
 ; APPLICANT: Shenk, Michael A.  
 ; APPLICANT: McGrath, Annette  
 ; APPLICANT: Glenn, Matthew  
 ; TITLE OF INVENTION: Compositions and Methods for the  
 ; FILE REFERENCE: 110000: Modification of Gene Transcription  
 ; CURRENT APPLICATION NUMBER: US/09/640,211A  
 ; CURRENT FILING DATE: 2000-08-16  
 ; NUMBER OF SEQ ID NOS: 2368  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 1731  
 ; LENGTH: 411  
 ; TYPE: DNA  
 ; ORGANISM: Pinus radiata  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1) .(411)  
 ; OTHER INFORMATION: n = A,T,C or G

US-09-640-211A-1731

Query Match 46.9%; Score 153.2; DB 3; Length 411;  
 Best Local Similarity 77.7%; Pred. No. 7e-43;  
 Matches 185; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 58 AAGCGCTTTGAGTGAaaaATGGAAATGCAGTAGGCCCTCTGGCTGGGATATTGGTT 117  
 Db 161 AACGTTTCGAAATCAGAACAGTGGAAATGCTTAGCCCTTGCGCTGGGATATTGGTT 220

Qy 118 GATAAAGTGGCACTTCAGGACCAATTTCAGGATTCATGAAATGTCAAAC 177  
 Db 221 GATAAATGGCACTTCAGAACCATCATGGACCTCTATTGTCAGGAAT 280

Qy 178 CAGGCGTCCGTACTTCAGAACAGTGAAGAATGCTACTGTCATGGGAAGTCTGTAACCATGCTTT 237  
 Db 281 CAAGCAGTGCACAACAGTCACTGTCATGGCTGGCTGCACTACGCCCTT 340

Qy 238 CACTTCACGTGATCTCGTGGCTAAACACGAAAGGGTGTCACTGGACACA 295  
 Db 341 CATTTCATTGCTAAAGTCGGTGGCTAAAGACGACAAAGTCTGCCATTAGATA 398

Qy 49 CGGGCAAGAAGCGCTTTGAGTGAaaaATGGAAATGCAGTAGGCCCTCTGGCTGGGATATTGGTT 108  
 Db 933 GCAGGACAGGAGGCTTGGTGGAAATGGCTGGCACTGGGATGGGAC 874

Qy 109 ATTGTGGTTGATAACTGTCGCACTGAGGACACATTGGATTTGTCATAGATGT 168  
 Db 873 GTAGCAGTGGCAACAGTGGCTTCAGCTGGCACTGGCTGGGATGGGATGGG 814

Qy 169 CAAGCTAACCGAGGCTGGTACTTCAGAAGAGTACTGTCGATGGGAAGTCTGTAAC 228  
 Db 813 CAGGGCACC---CGAATGCAAACCAAGACGAGTGCACTGTGGCTGGGAGTCAC 757

Qy 229 CATGCTTTCACTTCAGTCTCGCTGGCTAAACACGACAGGTGTTCATTGGCTGGG 288

Db 756 CAGGCTTCATTACCTGACATGGCTGGCTAAACACGACAGGTGTTCATTGGCTGGG 697

Qy 289 GACAAGAGAGTGGGAATTCCAAAAGTATGGCACTAG 327  
 Db 696 GACAACAGGAGTGGCTACAGAGTACGGCTGGCTGGGATGGGCTGGG 658

**RESULT 11**  
 US-09-270-767-26812/c  
 Sequence 26812 Application US/09270767  
 ; Patent No. 6703491

; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 11265  
 ; LENGTH: 1101  
 ; TYPE: DNA  
 ; ORGANISM: Drosophila melanogaster

US-09-270-767-11265

Query Match 42.3%; Score 138.2; DB 3; Length 1101;  
 Best Local Similarity 71.0%; Pred. No. 1.9e-37;  
 Matches 198; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

Qy 49 GCGGGAGAAGCGCTTTGAGTGAaaaATGGAAATGCAGTAGGCCCTCTGGCTGGGATATTGGTT 108  
 Db 933 GCAGGACAGGAGGCTTGGTGGAAATGGCTGGCACTGGGATGGGAC 874

Qy 109 ATTGTGGTTGATAACTGTCGCACTGAGGACACATTGGATTTGTCATAGATGT 168  
 Db 873 GTAGCAGTGGCAACAGTGGCTTCAGCTGGCACTGGCTGGGATGGGATGGG 814

Qy 169 CAAGCTAACCGAGGCTGGTACTTCAGAAGAGTACTGTCGATGGGAAGTCTGTAAC 228  
 Db 813 CAGGGCACC---CGAATGCAAACCAAGACGAGTGCACTGTGGCTGGGAGTCAC 757

Qy 229 CATGCTTTCACTTCAGTCTCGCTGGCTAAACACGACAGGTGTTCATTGGCTGGG 288

Db 756 CAGGCTTCATTACCTGACATGGCTGGCTAAACACGACAGGTGTTCATTGGCTGGG 697

Qy 289 GACAAGAGAGTGGGAATTCCAAAAGTATGGCACTAG 327  
 Db 696 GACAACAGGAGTGGCTACAGAGTACGGCTGGCTGGGATGGGCTGGG 658

**RESULT 13**  
 US-09-914-324A-4  
 Sequence 4 Application US/09914324A  
 ; Patent No. 6858709

; GENERAL INFORMATION:  
 ; APPLICANT: Conway, Joan A.  
 ; APPLICANT: Conway, Ronald C.  
 ; APPLICANT: Kamura, Takumi

Query Match 42.3%; Score 138.2; DB 3; Length 490;  
 Best Local Similarity 71.0%; Pred. No. 1.2e-37;  
 Matches 198; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

APPLICANT: Oklahoma Medical Research Foundation  
 TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor Complex and Sce Ubiquitin Ligase  
 FILE REFERENCE: 02104-004600US  
 CURRENT APPLICATION NUMBER: US/09/914,324A  
 PRIOR APPLICATION NUMBER: US 60/121,787  
 PRIOR FILING DATE: 2003-02-11  
 PRIORITY NUMBER: WO PCT/US00/04838  
 PRIOR FILING DATE: 2000-02-26  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Patentin ver. 2.1  
 SEQ ID NO: 4  
 LENGTH: 480  
 TYPE: DNA  
 ORGANISM: *Saccharomyces cerevisiae*  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (4)..(369)  
 OTHER INFORMATION: Rbx1  
 US-09-914-324A-4

Query Match 37.8%; Score 123.6; DB 3; Length 480;  
 Best Local Similarity 66.5%; Pred. No. 1.4e-32;  
 Matches 177; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
 Qy 55 AAGAAGCGCTTGAACTGAAAGTGGAAATGCACTGGCCCTGGGCTGGATATTG 114  
 Db 97 AAGAAGAATTTGAATTAAGAACCTGGATATGGTCAAGGATAATGCT 156  
 Qy 115 GTTGATAACTGTGCCATCTGGAAACACATTATGATCTTGGATAGATGCAAGCT 174  
 Db 157 GTTGACAACGTGCTTGCATTGAGAACATAATGAAACCATGATGTCAGCCA 216  
 Qy 175 ACCGGGGTCTGGTACTCTGAAAGAGTGTACTGTGGATCTGTAACCATGCT 234  
 Db 217 AAGGCCATGACGGACATGATAATGATGTTGAGCTGGGTCTTAATGCT 276  
 Qy 235 TTTCACTTCACTGATCTCTGGCTGCTCAAATACGACAGGTGTGCAATGGACAC 294  
 Db 277 TCCATTGCACTGATTAATGGATCAAGAACGCAATGCCATTAGATAAAC 336  
 Qy 295 AGAGAGTGGGAATTCAAAAGTATGG 320  
 Db 337 CAACCTGGAGATTCAAAAGTATGG 362

US-09-248-796A-5495

Sequence 5495, Application US/09248796A.  
 Patent No. 674137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

SEQ ID NO: 5495

LENGTH: 357

TYPE: DNA

ORGANISM: *Candida albicans*

US-09-248-796A-5495

Query Match 35.0%; Score 114.4; DB 3; Length 357;  
 Best Local Similarity 66.8%; Pred. No. 1.9e-29;  
 Matches 179; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

Qy 62 GCTTGTAAAGTGGAAATGCACTGGCCCTGGGATATTGGTTGATA 121  
 Db 89 GATTTGAACTGAAARATGGACGCGGTTGCTCATGGCAAAATGGAAA 148  
 Qy 122 ACTGTGCCATCTGGAGGACCAATTATGGATCTTGCATAGATGTAAGCTAA---CC 178  
 Db 149 ATTTGCTTGTGAAATTCATTAATGGAAACATGTTGATGTAACCAATGCTA 208  
 Qy 179 AGGGTCCGCTACTCAGAAGCTGTACTGTCGATGGGAGTCGTGAAACCAGCTTTC 238  
 Db 209 TGGGTAATATTCCITCAGAGAGTGTATCCTGGGAGATGTATCATCATTC 268  
 Qy 239 ACTTCACTGCACTGATCTCCCTGGTCAAAACACACAGTGTCCATTGGACAGAG 298  
 Db 269 ATTACATTTTATAGAATGTGTGAAACAAATCATGTCCTTGGATGTACTA 328  
 Qy 299 AGTGGAAATCCAAAGTATGGGACTA 326  
 Db 329 ATTGGACTATCAAATGGTATTAA 356

#### RESULT 15

US-09-949-016-16682

; Sequence 16682, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENNER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIORITY NUMBER: 60/241,755  
 ; PRIORITY FILING DATE: 2000-10-20  
 ; PRIORITY APPLICATION NUMBER: 60/237,768  
 ; PRIORITY FILING DATE: 2000-10-03  
 ; PRIORITY APPLICATION NUMBER: 60/231,498  
 ; PRIORITY FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 20712  
 ; SOFTWARE: Fastseq for Windows Version 4.0  
 ; SEQ ID NO: 16682.  
 ; LENGTH: 25274  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-16682

Query Match 28.3%; Score 92.6; DB 3; Length 25274;  
 Best Local Similarity 96.0%; Pred. No. 6.1e-21;  
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 221 TCTCTTAACCATGCTTTCACTTCACTGCACTCTCGCTGGCTCAAACACGACAGGTGT 280  
 Db 18403 TCTTCAGATGCTTTCACTTCACTGCACTCTCGCTGGCTCAAACACGACAGGTGT 18462  
 Qy 281 GTCATGGACAAAGAGTGGAAATGCAAAAGTCAAGATGTTCAAAGTATG 319  
 Db 18463 GTCTATGGACAAAGAGTGGAAATGCAAAAGTCAAGATGTTCAAAGTATG 18501

Search completed: March 8, 2006, 14:48:17  
 Job time : 100.735 secs